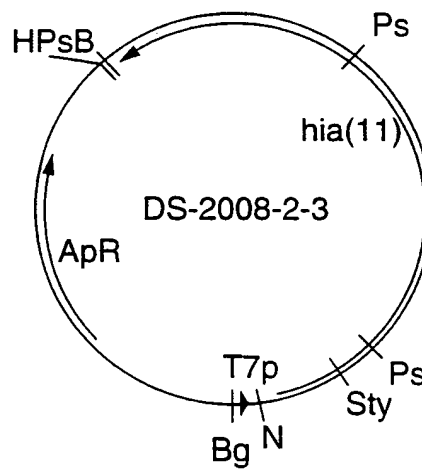


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Restriction map of DS-2008-2-3, pT7 hia (11).



pT7 hia (11)

FIG.1A

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FIG. 1B

# FIG. 1B

Oligonucleotides used to PCR amplify the full-length strain 11 hia gene for expression studies.

sense

EcoR I Nde I

5' GCGAATTCATATGAACAAAATTTTAAACGTTATTGGAAT 3' M N K I F N V I W N P

SEQ ID NO:2  
SEQ ID NO:1

5038.SL

antisense

5' AAAACAGCGGTTCACGAGGTGTGGTTACCACTGGTAATAG  
3' TTGTGCGCAACGTCGTCACACCAATGGTCACATTATCTAAGCCCTAGCG

SEQ ID NO:5  
SEQ ID NO:4  
SEQ ID NO:3

5039.SL

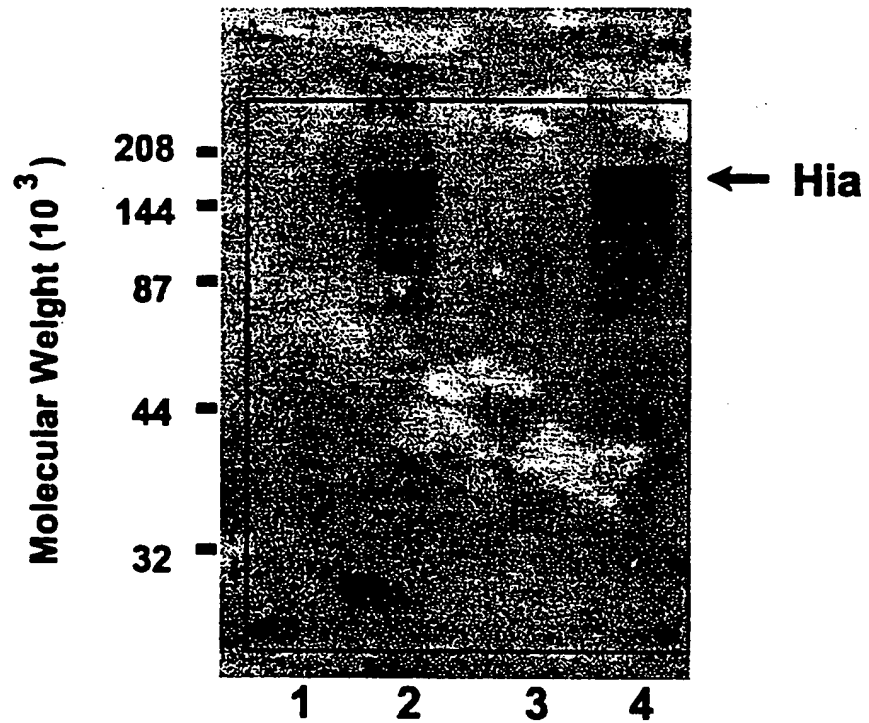
EcoR I BamH I

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FIG.2

FIG. 2



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Construction of DS-2092-1 and DS-2092-40,  
plasmids containing tandem T7 hia (11) genes.

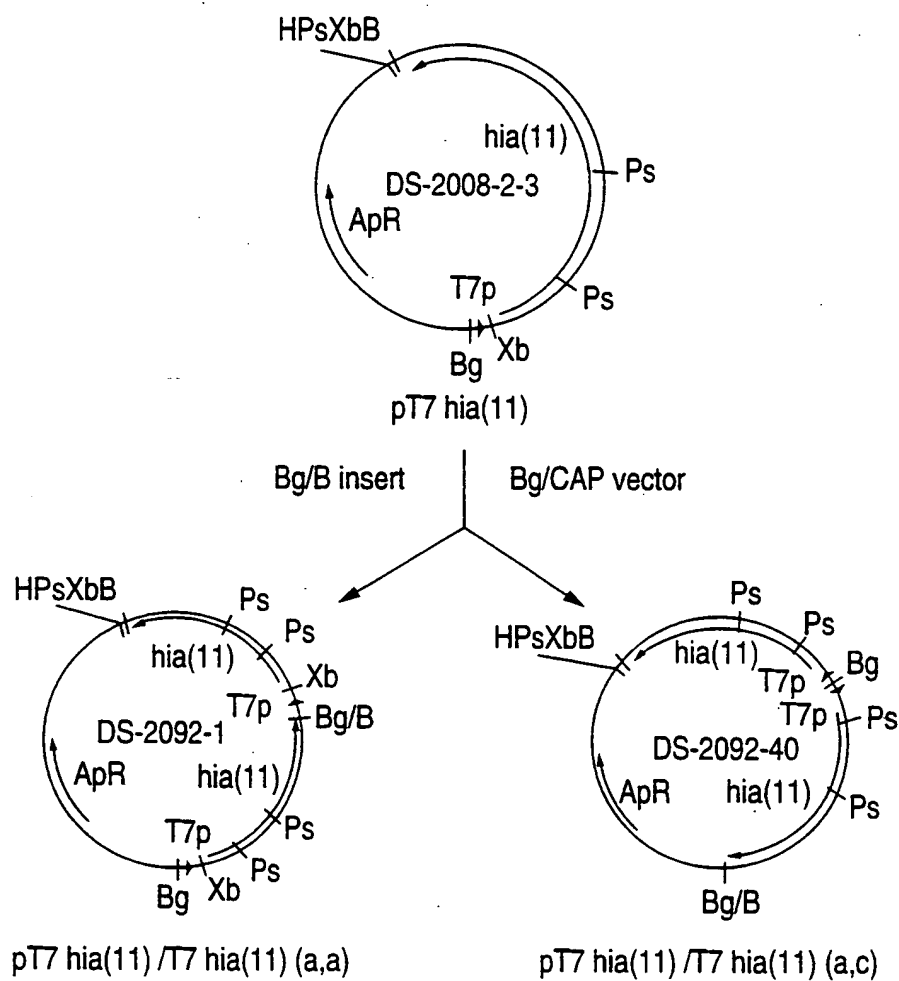


FIG.3

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FIG. 4

FIG.4

Sites for N-terminal truncations of rHia proteins.

MNKIFNVIMNVVITQIWVVSE<sup>21</sup>LIRTHHKCASAT<sup>33</sup>VAVAV<sup>38</sup>LATLLSATVEANAN<sup>52</sup>TFVINKLKAYGD (SEQ ID NO.6)

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Construction of plasmids expressing truncated hia (11) genes.

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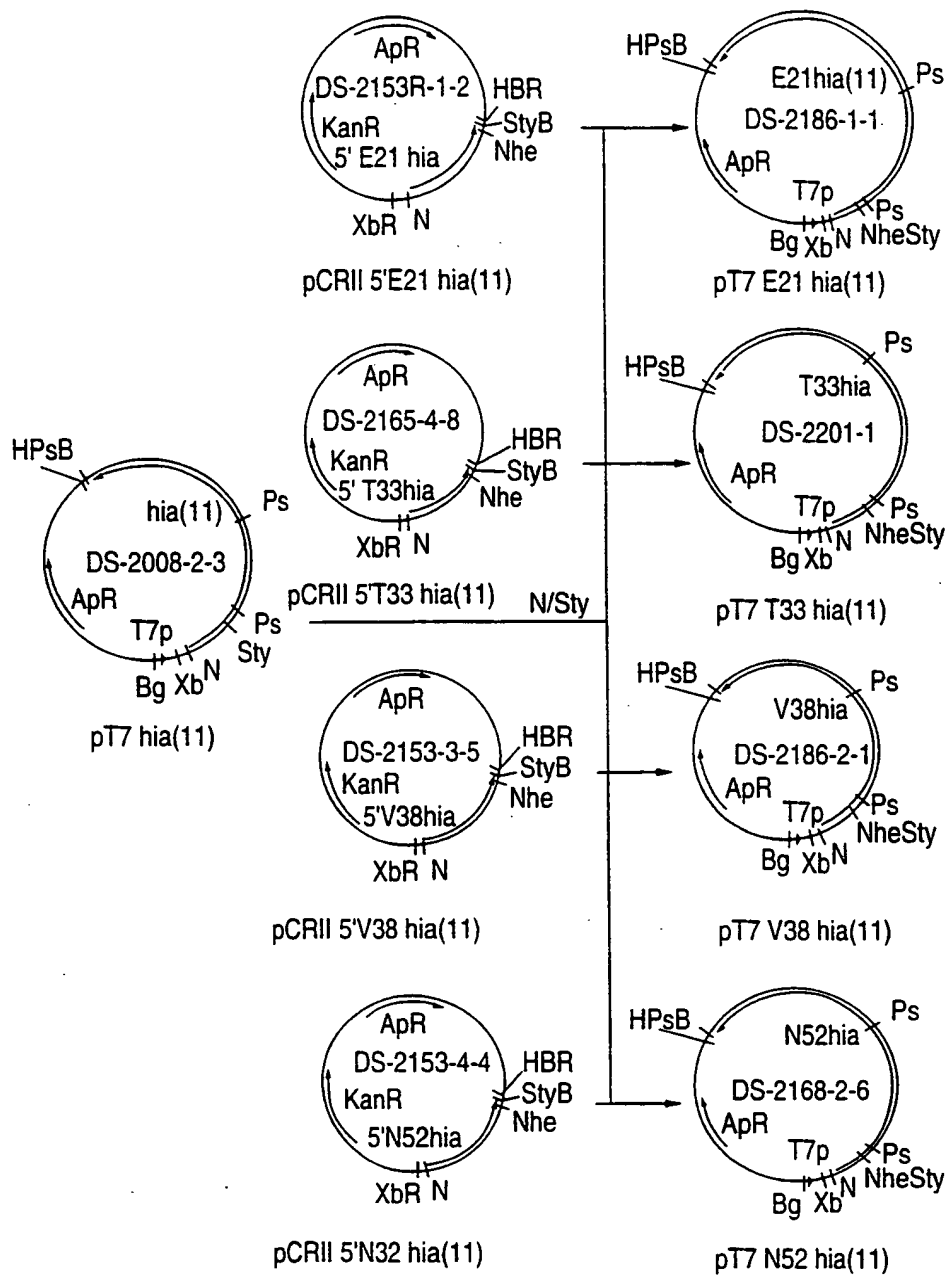


FIG.5A



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TOP SECRET

# FIG.5B

Oligonucleotide primers to PCR amplify truncated strain 11 *hla* genes.

E21	EcoR I Nde I ↓ ↓ M E L T R T H T K C A GGGAATTCATATGGAACCTCACTCCACCCACACCAATGGGC	5'	3'	5524.SL	SEQ ID NO: 8 SEQ ID NO: 7
T33	M T V A V A V L A T L GGGAATTCATATGACCGTGGCGGTTCGGTATGGCAACCTG	5'	3'	5525.SL	SEQ ID NO: 10 SEQ ID NO: 9
V38	M V L A T L L S A T GGGAATTCATATGTTATGGCAACCTGTGTCCCAACG	5'	3'	5526.SL	SEQ ID NO: 12 SEQ ID NO: 11

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FIG. 5B

FIG. 5B'

N52  
5' M N T P V T N K L K A 3' 5527.SL  
GGGAATTCATATGATACCTCTGTTACGAATAAGTTGAAGCTT SEQ ID NO:14  
SEQ ID NO:13

antisense

5' H T I T F A L A K D L G 3' SEQ ID NO:17  
CACACCATTTACCTTTTGGCTAGCGAAGACCTTGGTGG SEQ ID NO:16  
3' GTGTGTTAATGGAACCGGATCGCTTTCTGGAACCACTAGGCG 5' 5528.SL  
↑ Nhe I Sty I BamH I



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Construction of BK-96-2-11,  
a plasmid containing T7 V38 hia(11) and cer.

09/936362, 12/15/04

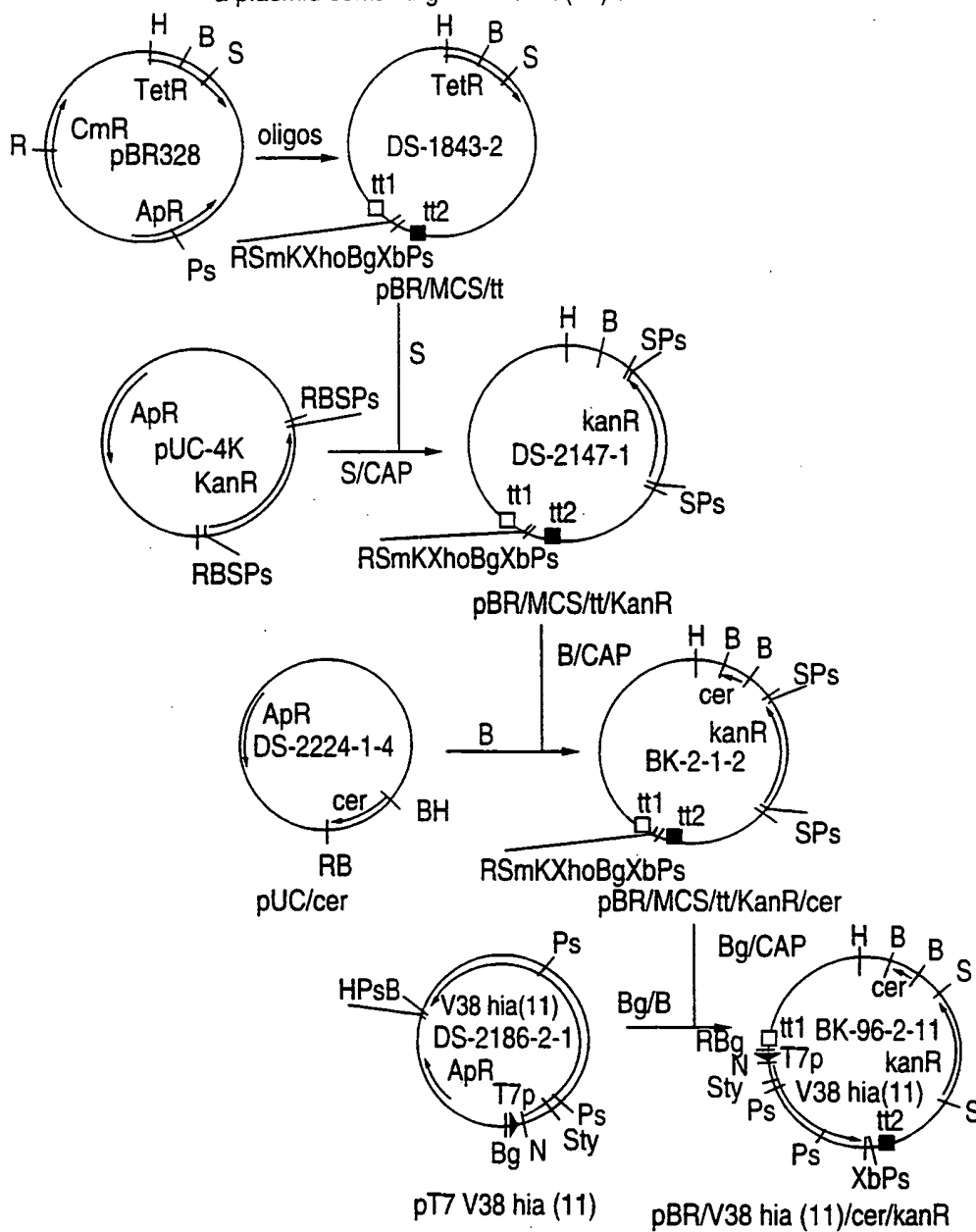


FIG.6A

Oligonucleotides used to generate the multiple cloning site and transcription terminators for the expression plasmids

"S"

SEQ	ID NO:50
SEQ	ID NO:51

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Construction of DS-2242-1 and DS-242-2,  
plasmids containing T7 hia (33) and cer.

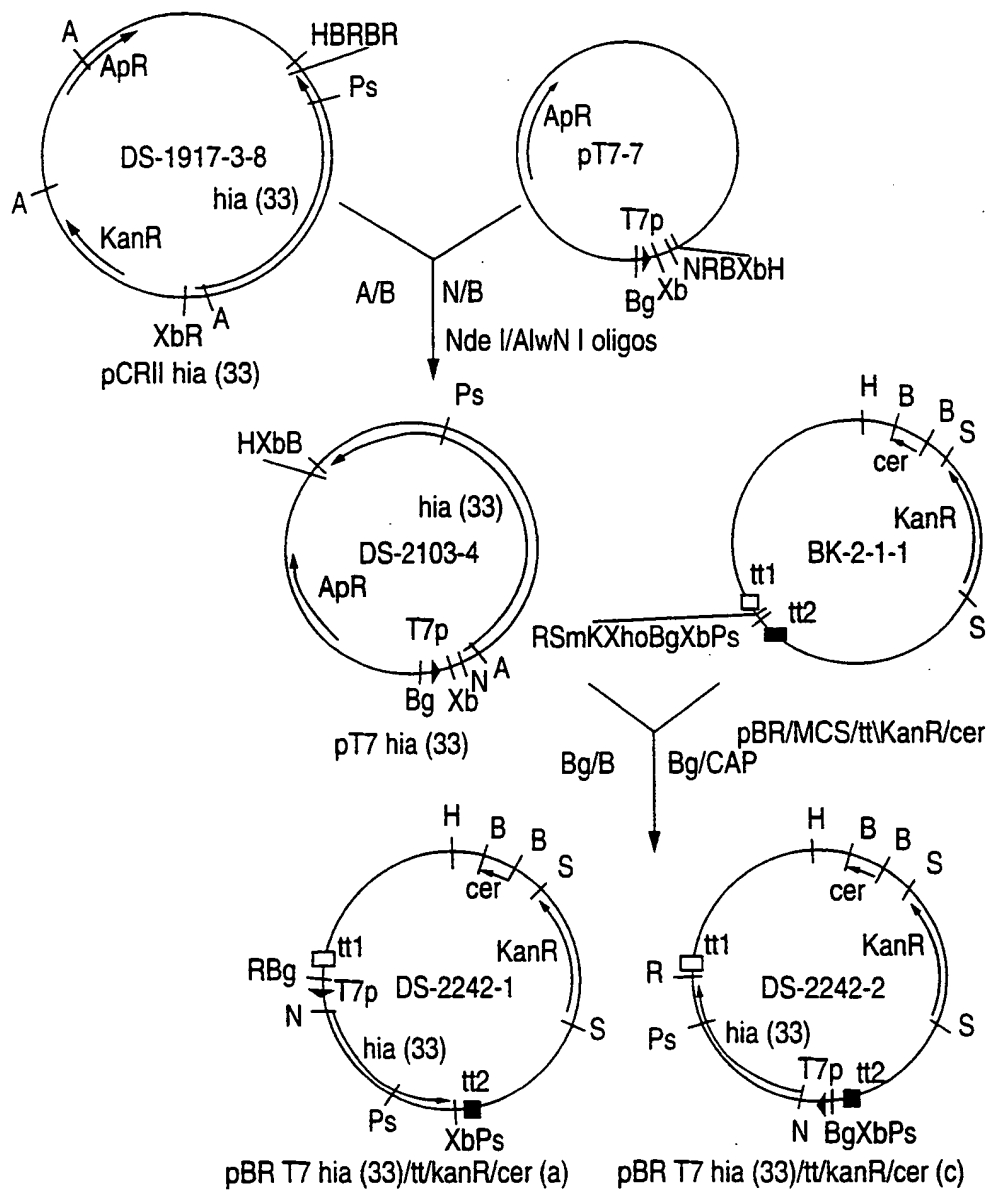


FIG.7A

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TTGTTT "29996666"

# FIG.7B

Oligonucleotides used to generate the 5'-end of the strain 33 hia gene for expression studies.

Nde I  
↓  
M N K I F N V I W N V M T Q T W A V V S E L T R A H T K...  
TATGAACAAAATTTTAAACGTTATTTGGAAATGTTATGACTCAAACTTGGGCTGTCG  
TATCTGAAC TCACTGCGGCGCCACACCA...  
ACTTGTTTTAAAAATTGCAATAAACCTTACAATACTGAGTTT  
GAACCGACACATAGACTTCAGTGAGCGCGGCTGTGGT...  
... R A S A T V A A SEQ ID NO:54  
...AACGTGCTCCCTCCGCAACCGTGGCAGCCG SEQ ID NO:52  
...TTGCACGGAGCGGTTGGCACCGTC SEQ ID NO:53  
...  
AlwN I



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Construction of DS-2340-2-3,  
a plasmid containing T7 V38 hia (33) and cer.

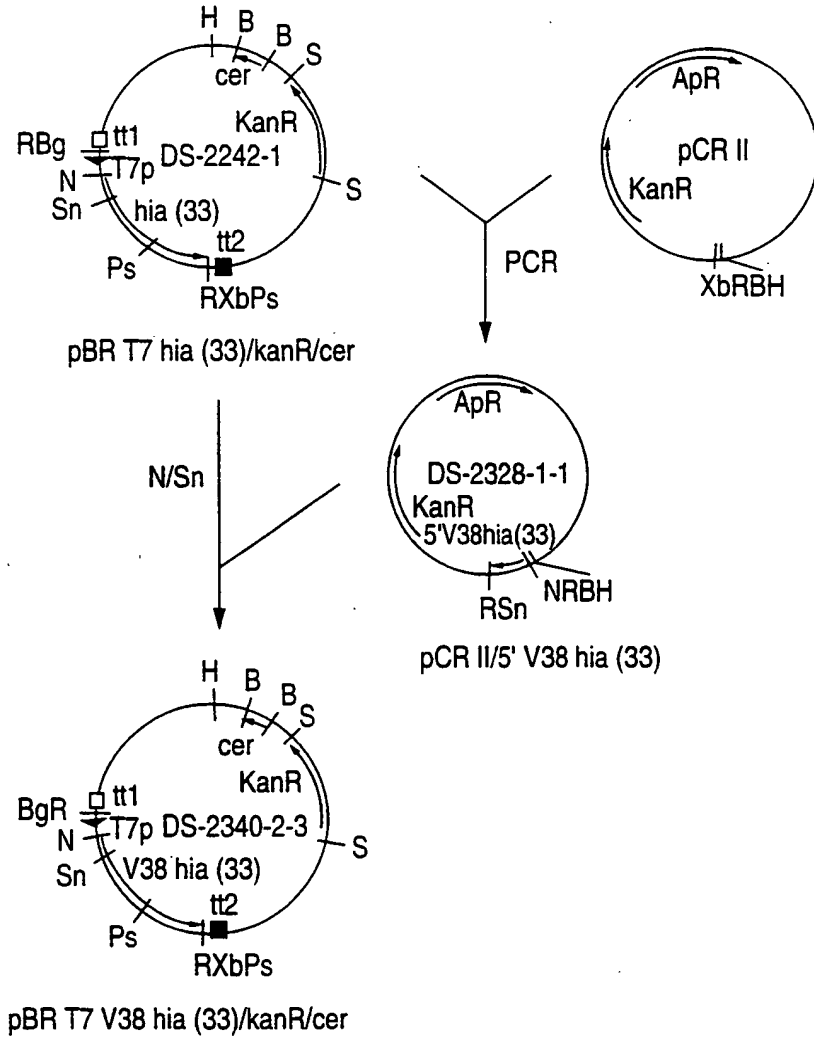


FIG.8A

[illegible]

oligonucleotides used to PCR amplify the strain 33 *hla* gene from the V38 codon to the SnaB I site.

6286.SL

D E T T A T V G N L R K L  
GACGAACCAACGCAACGTAGGCAATTACGTAAATGACCTCG  
CTGCTTTGGGGGTTGCATCGTTAATGCATTACCTCGAAGC

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Construction of DS-2447-2,  
a plasmid containing tandem T7 V38 hia (11) cassettes and cer.

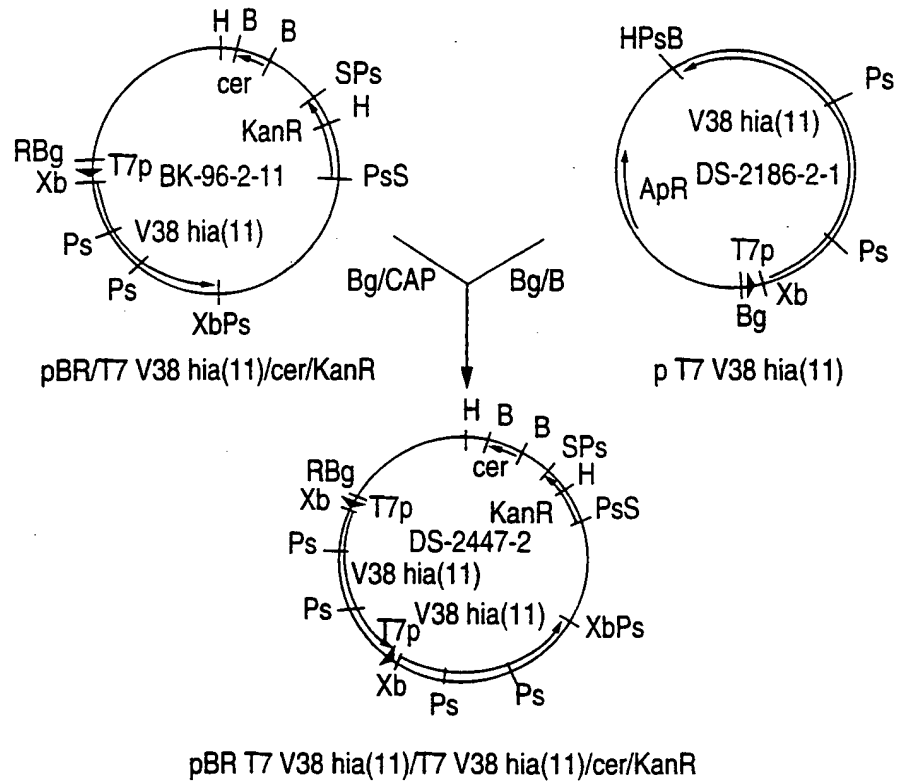


FIG.9A

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Construction of DS-2448-17,  
a plasmid containing tandem T7 V38 hia(33) cassettes and cer.

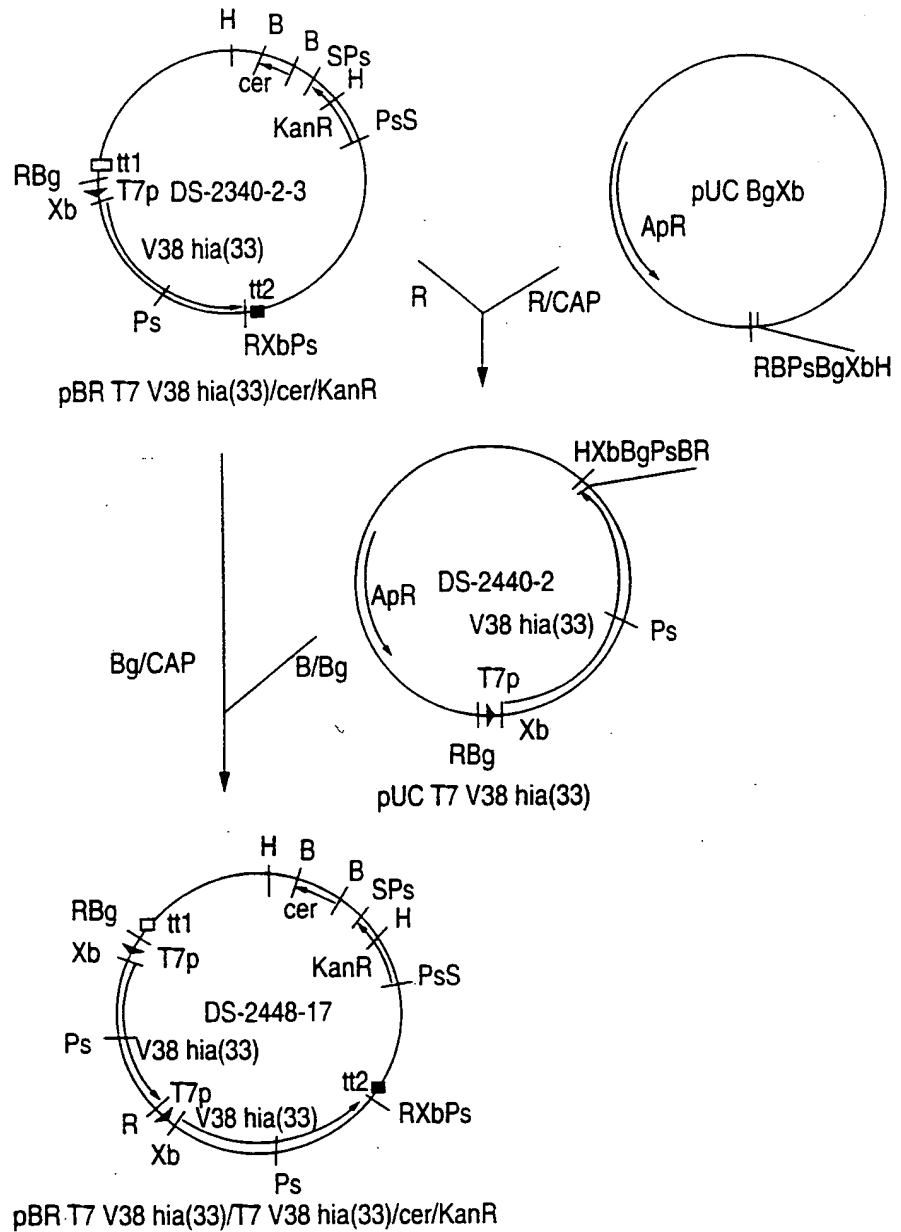
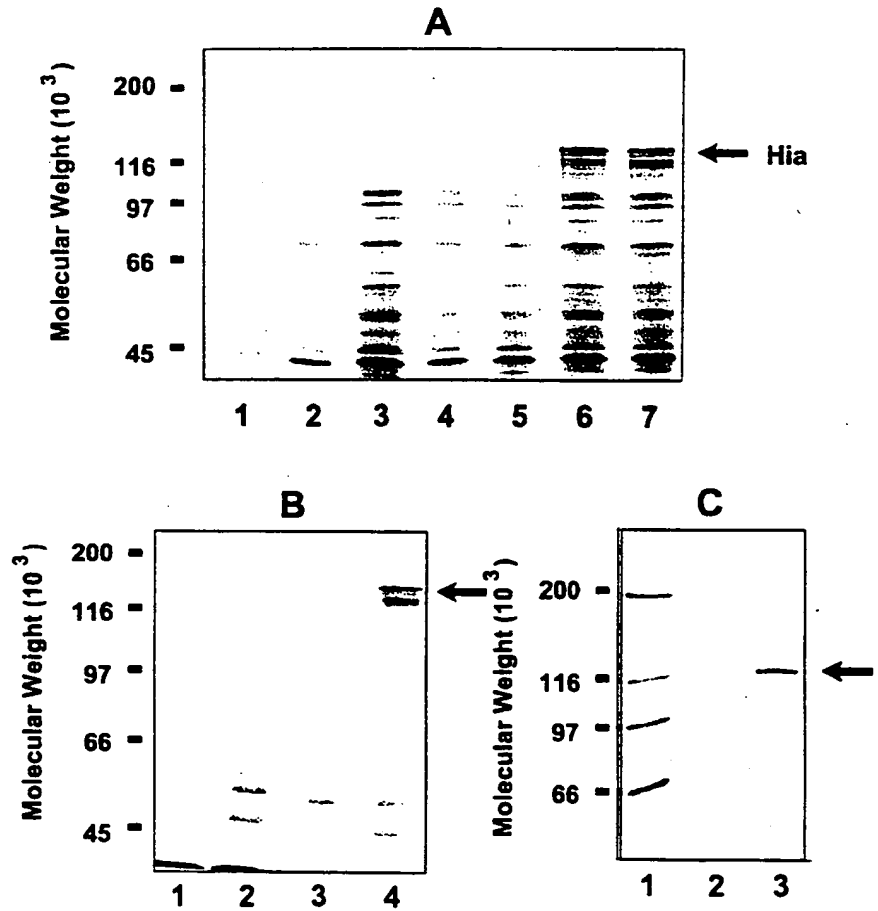


FIG.9B



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FIG.10



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Purification of rHia Proteins from E. coli

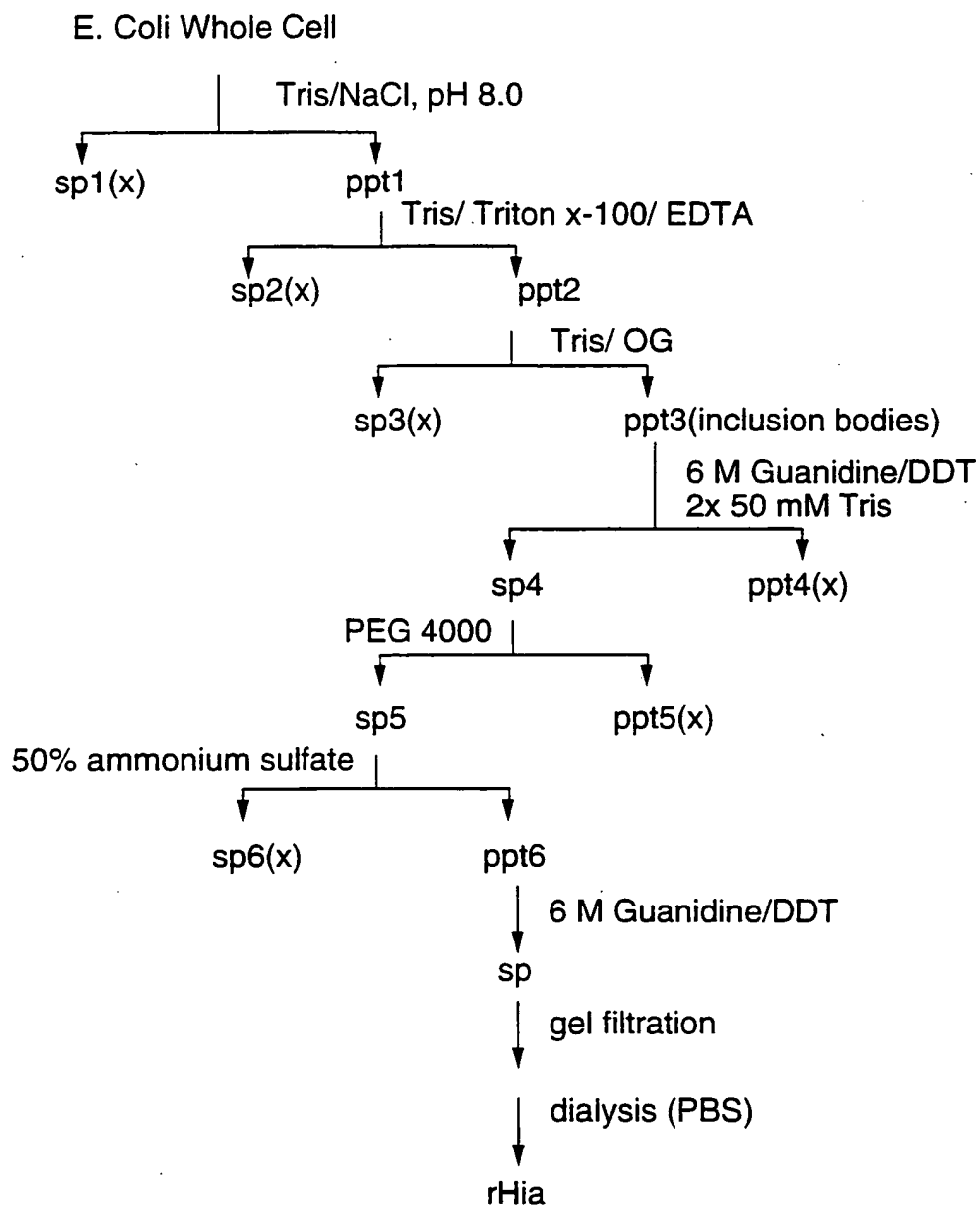
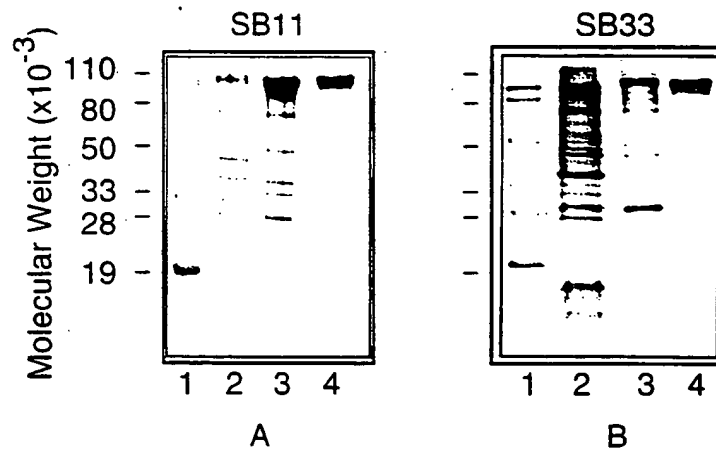


FIG.11

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Purification of rHia (V38) from E. coli



1. Prestained molecular weight markers
2. E. coli whole cell lysate
3. Crude extract
4. Purified rHia protein

FIG.12

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The Stability of rHia (V38/SB11)

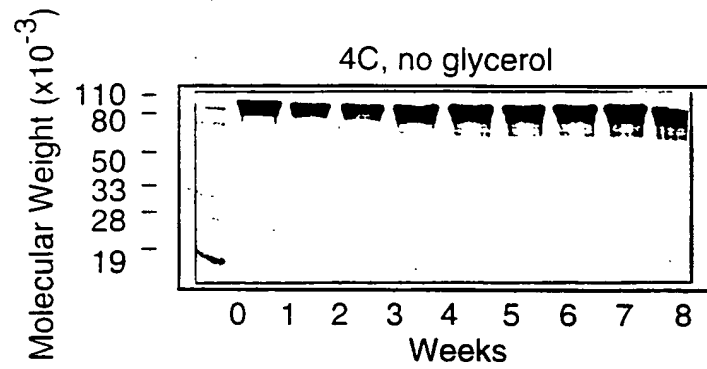


FIG.13A

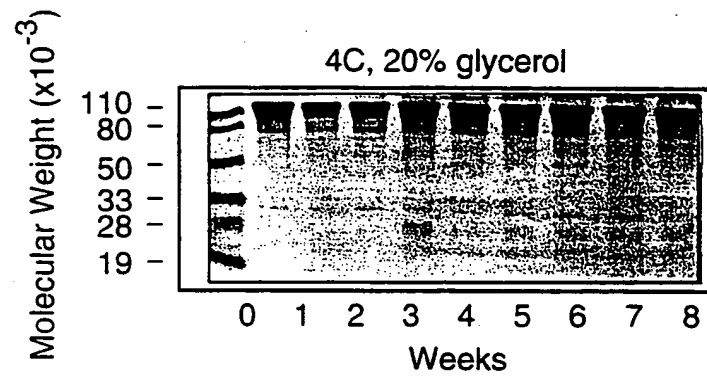


FIG.13B

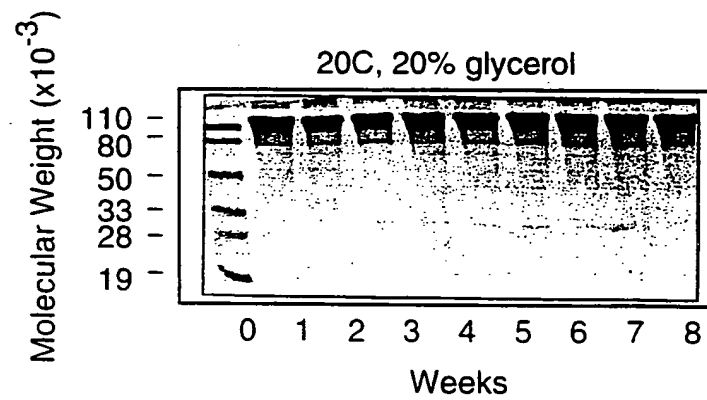


FIG.13C

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# Anti-rHia (V38) Antibody Titers in Mice

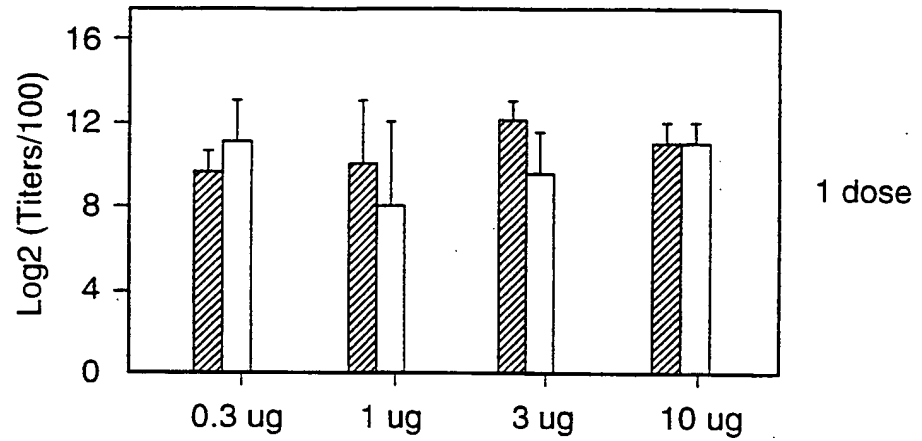
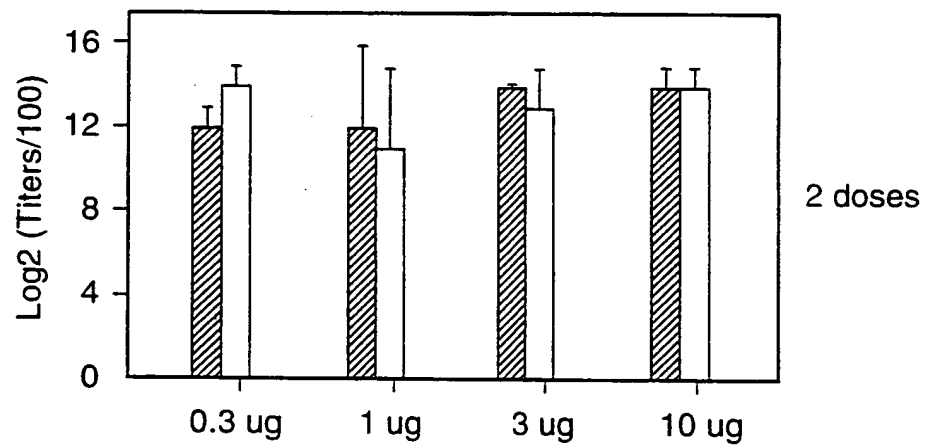


FIG.14A



SB11  
SB33

FIG.14B

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Anti-V38 rHia (SB11) Antibody Titers in BALB/c Mice

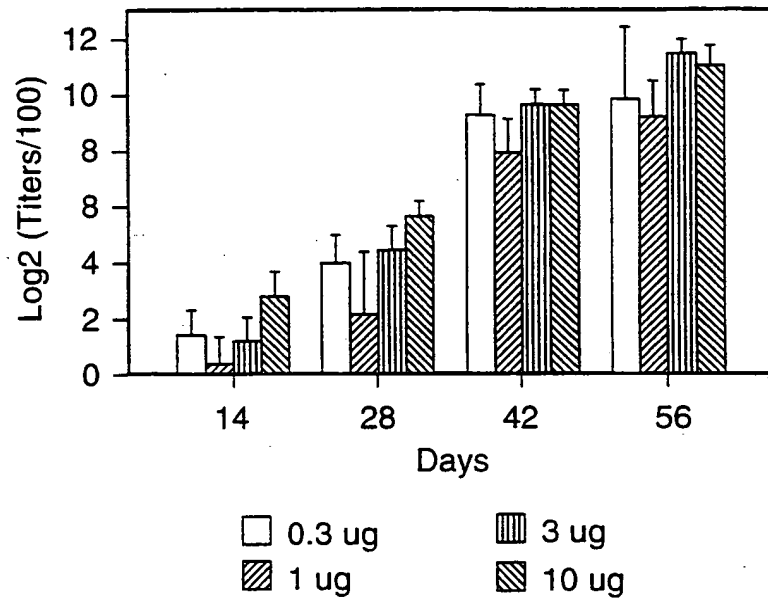


FIG.15A

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Anti-V38 rHia (SB11) Antibody Titers in Guinea Pigs

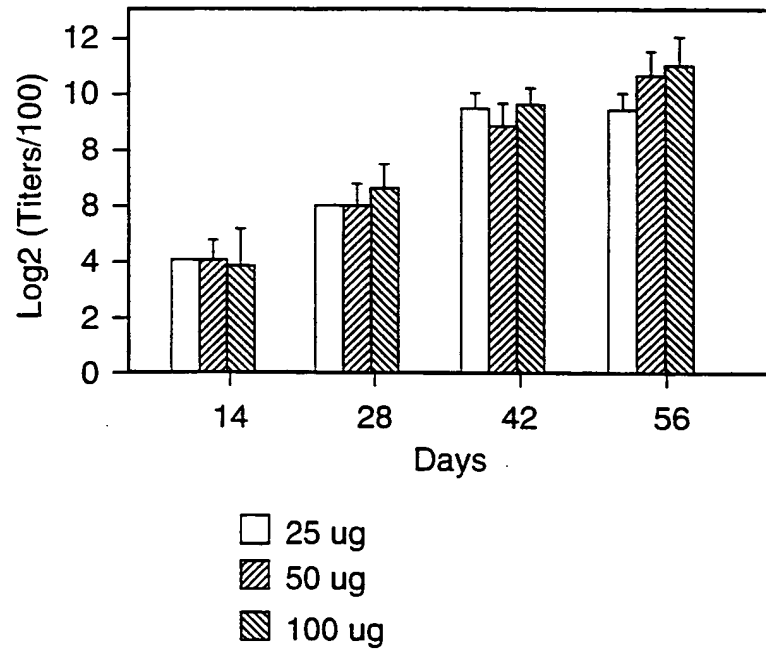


FIG.15B

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FIG. 16

Protective Ability of rHia (V38/SB33) Against  
NP Colonization with NTHi Strain 33 in Chinchillas

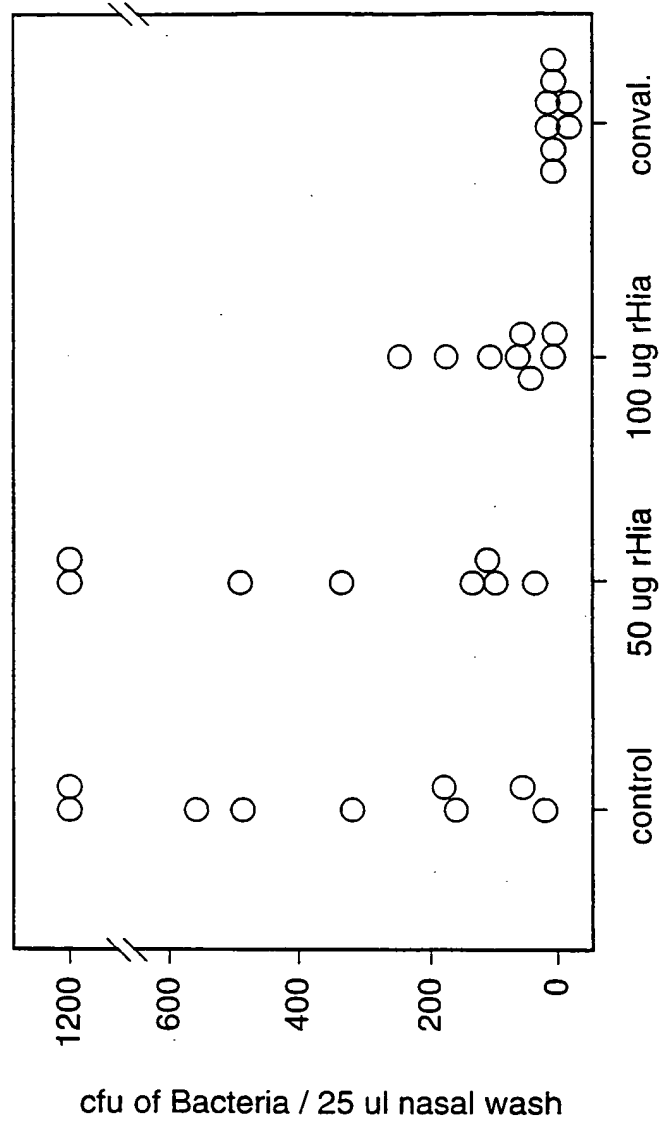


FIG.16



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FIG.17

Oligonucleotides used to PCR amplify additional *hia* genes.

sense

5' TTAATATAAGGTAAATAAAATGACAAATTTTAAAGTT 3' 5040.SL  
M N K I F N V  
SEQ ID NO:22  
SEQ ID NO:21

antisense

5' AAAACAGCGGTTGCAGCAGGTTGGTTACCAAGTGTAAATAG 3'  
3' TTTTGTCGCAACGTCGTGTCACAAACCAATGGTCACCAATTATCTTAAGCGCTAGCGG 5' 5039.SL  
K T G V A A G V G Y Q W \* \*  
↑ ↑  
EcoR I BamH I

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SEQ ID NO:5  
SEQ ID NO:4  
SEQ ID NO:3

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TABLE "29592500"

FIG.18A

NH1 strain 33 Hia

GAATTCGGCTTAAATAAAATGAACAA...	10	MET ASN LYS...	20	... ILE PHE ASN VAL ILE TRP ASN VAL MET THR GLN	30	... AATTTTAAACGTTATTGGAATGTTATGACTCA	40	... 50	60
THR TRP ALA VAL VAL SER GLU LEU THR...	70	... ARG ALA HIS THR LYS ARG ALA SER ALA THR VAL	80	... TCGCGCCACACCAACGTCCTCCGCAACCGT	90	... 100	110	120	
AACTTGGGCTGTCGTATCTGAACCTCAC...	130	ALA ALA ALA VAL LEU ALA THR VAL LEU...	140	... SER ALA THR VAL GIN ALA SER ALA GLY SER THR	150	... GTCGTGCAACGGTTTCAGGCGAGTGCGAGGCAGTAC	160	170	180
GCAGCCGCTGTATTGGCGGACCGTATT...	190	THR GLY THR ASN SER LEU ASN VAL TYR...	200	GACAGGTACAAATAGTTTGAATGTTTA...					

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FIG.18B

105721 2999660

... GLY LYS ASN ASN SER ASN PHE ASN SER ALA ASN  
...TGGAAAGAAATAATTCCGAATTTCATTTCAGCCAA 240  
... 210 220 230

ASN SER ILE ALA ASP LEU ASN LYS GLN...  
TAATTCAATAGCAGATTATAATAACA... 250  
... 260  
... ASN ASP SER VAL TYR ASP GLY LEU ASN LEU  
...AATGATAGTGTTTACGATGGTTTATTATAATCT 300  
... 270 280 290

ASN GLU LYS GLY THR ASP LYS SER LYS...  
GAATGAAAGGACGATAGTCAA... 310  
... 320  
... PHE LEU VAL ALA ASP GLU THR ALA THR VAL  
...ATTCTGGTTGCTGACGAAACCAACCGCAACCGT 360  
... 330 340 350

GLY ASN LEU ARG LYS LEU GLY TRP VAL...  
AGGCAATTACGTAATAATTGGGTTGGGT... 370  
... 380  
... VAL SER THR LYS ASN SER THR LYS GLU SER  
...AGTATCAACCAAAACACAGTACGAAAGAAAG 420  
... 390 400 410

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FIG. 18C

FIG. 18C

ASN GLN VAL LYS GLN ALA ASP GLU VAL...  
CAATCAAGTCAACACAGCGGATGAAGT...  
430 440  
... LEU PHE GLU GLY LYS ASP GLY VAL THR VAL THR  
...GTTGTTTGAAGGCAAGACGGGTGTAACGGTTAC  
450 460 470 480

SER LYS SER GLU ASN GLY LYS HIS THR...  
TTCCAAATCTGAACACGGGCAACACAC...  
490 500  
... VAL THR PHE ALA LEU ALA ASN ASP LEU ASN VAL  
...CGTTACTTTTGGCCCTTGCCGAATGACCTTAATGT  
510 520 530 540

LYS ASN ALA THR VAL SER ASP LYS LEU...  
AAAAACGCAACCGTTAGCGATAAATT...  
550 560  
... SER LEU GLY ALA ASN GLY LYS VAL ASP ILE  
...ATCGCTTGGTGCAACACGGCAAGAAAGTCGATAT  
570 580 590 600

THR SER ASP ALA ASN GLY LEU LYS PHE...  
TACCAAGTGAATGCAACACGGCTTGAAATT...  
610 620

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TTGTTAT\*24E9E66D

FIG.18D

... ALA LYS GLN GLY THR ASN GLY GIN GLN GLY ASN GLY ASN  
...T GCGAAACAGGGTACGAAATGGGTCAAACACGGTAA 660  
... 630 640 650

VAL HIS LEU ASN GLY ILE ALA SER THR...  
TGTTCACCTTAAACGGGTATTGCTTCGAC... 680  
... LEU ASP ASP PRO ARG VAL GLY GLY LYS THR ALA  
...TTAGATGATCCCTCGTGTTGGGTGGAAACACAGC 720  
... 690 700 710

HIS LEU THR LYS GLU ILE SER ASP THR...  
ACACCTTACAAAGAAATCAGCGATAC... 740  
... GLU ARG ASN ARG ALA ALA SER VAL GLY ASP VAL  
...AGACGTAACCGTGCTGCCGAGCGTGGGCGGATGT 780  
... 750 760 770

LEU ASN ALA GLY TRP ASN ILE ARG GLY...  
ATTGAATGCGGGGTTGGAAATATTCTGTGG... 800  
... ALA LYS THR ILE GLY GLY THR VAL ASP ASN VAL  
...CGCAAAACGATTGGCGGTACAGTGGATAATGT 840  
... 810 820 830

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FIG. 18E

FIG. 18E

ASP PHE VAL SER THR ASP THR VAL...  
TGATTTTGTTCACACTTATGACACTGT...  
850  
... GLU PHE ALA SER GLY ALA ASN ALA ASN VAL SER  
...TGAATTGCCAGCGCGCAACGCAAAATGTGAG  
... 870 880 890 900

VAL THR THR ASP ASP ASN LYS LYS THR...  
CGTTACGACTGATGATAACAAATAAAC...  
910  
... THR VAL ARG VAL ASP VAL THR GLY LEU PRO VAL  
...AACCGTCCGTGTGGATGTACAGGCTTGCCGGT  
... 930 940 950 960

GLN TYR VAL THR GLU ASP SER LYS THR...  
CCAATATGTTACGGGAAGACAGCAAAAC...  
970  
... VAL VAL LYS VAL GLY ASN GLU TYR GLU ALA  
...CGTTGTGAAGTGGGCAATGAGTATTACGAAGC  
... 990 1000 1010 1020

LYS GLN ASP GLY SER ALA ASP MET ASP...  
CAGCAAGACGGTTCGGCGGATATGGA...  
1030 1040

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FIG.18F

FIG.18F 24E9E60

... LYS LYS VAL GLU ASN GLY LYS LEU ALA LYS THR  
...TAA A A A G T C G A A A T G G C A A G C T G G C G A A A C  
... 1050 1060 1070 1080

LYS VAL LYS LEU VAL SER ALA ASN GLY...  
TAAAGTGAAATTGGGTATCGGCAACGG...  
1090 1100  
... THR ASN PRO VAL LYS ILE SER ASN VAL ALA ASP  
...TACAAATCCGGTGAAATCAGCAATGTTGCCGA  
... 1110 1120 1130 1140

GLY THR GLU ASP THR ASP ALA VAL SER...  
CGGCACGGAGATACCGATGCCGGTCAG...  
1150 1160  
... PHE LYS GLN LEU LYS ALA LEU GLN ASP LYS GLN  
...CTTAAAGCAGTTGAAAGCCCTTGCAAGATAACA  
... 1170 1180 1190 1200

VAL THR LEU SER ALA SER ASN ALA TYR...  
GGTTACGTTAAGTCCGAGCAATGCTTA...  
1210 1220  
... ALA ASN GLY SER ASP ALA ASP GLY LYS  
...TGCCCAATGGCGGTAGCGATGCCGACGGCGGCA  
... 1230 1240 1250 1260

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TOP OF "289566"

FIG.18G

ALA THR GLN THR LEU GLY ASN ASP LEU...  
GGCAACTCAAACTTTAGGCAATGATTT...  
1270  
... ASN PHE LYS SER THR ASP SER GLU LEU  
...GAAATTTTAAATTTAAATCCACAGACAGCGAGTT  
1280  
... 1290 1300 1310 1320

LEU ASN ILE LYS ALA ALA GLY ASP THR...  
GTTGAACATCAAGCAGCAGGTGACAC...  
1330  
... VAL THR PHE THR PRO LYS LYS GLY SER VAL GIN  
...GGTTACCTTTACGCCGAAATAAGGTTTCGGTGCA  
1340  
... 1350 1360 1370 1380

VAL GLY ASP ASP GLY LYS ALA THR ILE...  
GGTTGGCGATGATGGTAAGGCTACGAT...  
1390  
... GIN ASP GLY ALA LYS THR THR THR GLY LEU VAL  
...TCAAGACGGCGGAAACAACAATAACCGGTTTGGT  
1400  
... 1410 1420 1430 1440

GLU ALA SER GLU LEU VAL ASP SER LEU...  
TGAGGCTTCTGAATTGGTTGACAGCCT...  
1450  
... 1460

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FIG.18H

TOGETHER 2999566

... ASN LYS LEU GLY TRP LYS VAL GLY VAL GLY LYS  
...G A A C A A A T T G G C T G G A A A G T G G C G T T G G T A A  
... 1470 1480 1490 1500

ASP GLY THR GLY ALA THR ASP GLY THR...  
A G A C G G C A C A G G A G C C G A T G G C A C ...  
1510 1520 ...  
... HIS THR ASP THR LEU VAL LYS SER GLY ASP LYS  
...G C A T A C C G A C A C T T T A G T G A A G T C G G C G A T A A  
... 1530 1540 1550 1560

VAL THR LEU LYS ALA GLY ASP ASN LEU...  
A G T A A C T T T G A A A G C C G G C G A T A T C T ...  
1570 1580 ...  
... LYS VAL LYS GLN GLU GLY THR ASN PHE THR TYR  
...G A A G G T C A A C A A G A G G G T A C A A C T T C A C T A  
... 1590 1600 1610 1620

VAL LEU ARG ASP GLU LEU THR GLY VAL...  
C G T G C T C A G A G A T G A A T T G A C G G C G T ...  
1630 1640 ...  
... LYS SER VAL GLU PHE LYS ASP THR GLU ASN GLY  
...A A G A G C G T G G A G T T T A A G A C A C G G A G A A T G G  
... 1650 1660 1670 1680

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TTTTT" 29E9E6E0

FIG.18I

ALA ASN GLY ALA SER THR LYS ILE THR...  
TGCAACGGTGCAAGCACGAAAGATTAC...  
1690  
... LYS ASP GLY LEU THR ILE THR PRO ALA ASN ASP  
...CAAAGACGGCTTGACCATTCAGCCGGCAAACGA  
1700 1710 1720 1730 1740

ALA ASN GLY ALA ALA THR ASP ALA...  
TGCGAATGGTGCGGCGGCGACTGATGC...  
1750  
... ASP LYS ILE LYS VAL ALA SER ASP GLY ILE SER  
...TGACCAAGATTAAAGTGGCTTCAGACGGCATTAG  
1760 1770 1780 1790 1800

ALA GLY ASN LYS ALA VAL LYS ASN VAL...  
TGCGGGTAATAAGCAGTTAAACGTT...  
1810  
... VAL SER GLY LEU LYS LYS PHE GLY ASP ALA ASN  
...TGAGCGGACTGAAGAAATTTGGTGATGCCGA  
1820 1830 1840 1850 1860

PHE ASN PRO LEU THR SER SER ALA ASP...  
TTTCAATCCGCTGACTAGCTCAGCCGA...  
1870 1880

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TABLET "2999660"

FIG.18J

... ASN LEU THR LYS GLN TYR ASP ASN ALA TYR LYS  
...CAACTTAACGAAACAATAATGACCAATGCCCTATAA  
... 1890 1900 1910 1920

GLY LEU THR ASN LEU ASP GLU LYS SER...  
AGGCTTGACCAATCTGGATGAAAG...  
... 1930 1940  
... LYS GLY LYS GLN THR PRO THR VAL ALA ASP ASN  
...TAAGGCAAGCAAACTCCGACCGTTGCTGACAA  
... 1950 1960 1970 1980

THR ALA ALA THR VAL GLY ASP LEU ARG...  
TACCGCTGCAACCGTGGGCGATTGCG...  
... 1990 2000  
... GLY LEU GLY TRP VAL ILE SER ALA ASP LYS THR  
...CGGTTTGGGCTGGGTCAATTTCTGACAGCAAAAC  
... 2010 2020 2030 2040

THR GLY GLU SER LYS GLU TYR SER ALA...  
CACAGGCGAGTCAAGGAATATAGCGC...  
... 2050 2060  
... GLN VAL ARG ASN ALA ASN GLU VAL LYS PHE LYS  
...GCAAGTGCGTAACGCCCAATGAAGTGAATTCAA  
... 2070 2080 2090 2100

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FIG. 18K

FIG. 18K

SER GLY ASN GLY ILE ASN VAL SER GLY...  
GAGCGGCAACGGTATCAATGTTTCCGG...  
2110  
... LYS THR LEU ASP ASN GLY THR ARG GLU ILE THR  
...TAAACAATTGGATAACGGTACGGCGGAATTAC  
... 2130 2140 2150 2160

PHE GLU LEU ALA LYS ASP GLU ASN ALA...  
TTTGAATTGGCTAAAGACGAAATGC...  
2170  
... ILE ALA PHE GLY SER LYS ALA LEU ARG  
...CATTGCTTTCGGTTCTGGCTCAAAAGCCCTTGCG  
... 2190 2200 2210 2220

ASP ASN THR VAL ALA ILE GLY THR GLY...  
CGATAACACGGTGGCGATTGGTACGGG...  
2230  
... ASN VAL VAL ASN ALA GLU LYS SER GLY ALA PHE  
...CAACGTTGTGAATGCGGAAATACTGGTGCAATT  
... 2250 2260 2270 2280

GLY ASP PRO ASN TYR ILE GLU ASP LYS...  
CGCGGATCCGAACCTACATCGAAGATAA...  
2290 2300

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FIG.18L

TTTATTTTGGGCTT

... ALA GLY GLY SER TYR ALA PHE GLY ASN ASP ASN  
...AGCCGGTGGCAGCTACGCTTTCGGTAACGATAA 2340  
... 2310 2320 2330

ARG ILE THR SER LYS ASN THR PHE VAL...  
CCGTATTACTTCTTAAACACACTTTTGT... 2350  
... 2360  
... LEU GLY ASN GLY VAL ASN ALA LYS TYR LYS ALA  
...GTGGGTAATGGAGTTAATGCCGAAATATAAGC 2400  
... 2370 2380 2390

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ASN GLY ASP VAL ASP THR GLU THR VAL...  
CAATGGAGATGTTGATACCGAACAACCGT... 2410  
... 2420  
... THR VAL LYS ASP LYS ASP GLY LYS GLU THR THR  
...AAGTGTTAAGGACACAAGACGGTAAGAGACTAC 2460  
... 2430 2440 2450

VAL THR VAL PRO LYS ALA LEU GLY ALA...  
CGTTACTGTTCCCTAAAGCGGTTAGGGGC... 2470  
... 2480  
... THR VAL GLU ASN SER VAL TYR LEU GLY ASN LYS  
...TACGGTTGAAACACTCCGTTTATTGGGTAATAA 2520  
... 2490 2500 2510

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FIG.18M

SER THR ALA THR LYS ASP LYS GLY LYS...  
ATCGACTGCGGACAAAGATAAGGGTAA...  
2530  
... ASN LEU LYS SER ASP GLY THR ALA GLY ASN THR  
...AATCTGAATCTGATGGTACGGCGGGTAAACAC  
2540  
... 2550 2560 2570 2580

THR THR ALA GLY THR THR GLY THR VAL...  
TACAACTGCTGGTACACAGGGGTACGGT...  
2590  
... ASN GLY PHE ALA GLY ALA THR ALA HIS GLY ALA  
...AACGGCTTTGCCGGTGCAACGGCGCACGGGTGC  
2600  
... 2610 2620 2630 2640

VAL SER VAL GLY ALA SER GLY GLU...  
GGTTCTCTGCGCGCAAGCGCGGAAGA...  
2650  
... ARG ARG ILE GLN ASN VAL ALA GLY GLU ILE  
...AGACGTATCCAAACGTTGCCGCAAGCGGAAT  
2660  
... 2670 2680 2690 2700

SER ALA THR SER THR ASP ALA ILE ASN...  
TCCGGCTACTTCCACCGATGCGATTAA...  
2710  
... 2720

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FIG.18N

... GLY SER GIN LEU TYR ALA VAL ALA LYS GLY VAL  
...CGGCAGCCAGTTGTATGCCCGTGGCAAAAGGGGT 2760  
... 2730 2740 2750

THR ASN LEU ALA GLY GIN VAL ASN LYS...  
AACAAACCTTGCTGGACCAAGTGAAATAA... 2770  
... 2780

... VAL GLY LYS ARG ALA ASP ALA GLY THR ALA SER  
...AGTGGGCAAAACGTGCAGATGCAGGTACAGCAAG 2820  
... 2790 2800 2810

ALA LEU ALA ALA SER GIN LEU PRO GIN...  
TGCAATTAGCGGCTTCACAGTTACCACA... 2830  
... 2840

... ALA SER MET SER GLY LYS SER MET VAL SER ILE  
...AGCCTCTATGTCAGGTAAATCAATGTTTCTAT 2880  
... 2850 2860 2870

ALA GLY SER SER TYR GIN GLY GIN SER...  
TCCGGGAAGTAGTTATCAAGGTCAAAG... 2890  
... 2900

... GLY LEU ALA ILE GLY VAL SER ARG ILE SER ASP  
...TGGTTTAGCTATCAGGGGTATCAAGAAATTTCCGA 2940  
... 2910 2920 2930

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[illegible][illegible]

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FIG. 19A

FIG. 19A

NH1 strain 32 hia

G A A T T C G G C T T T A A A T A T A A G G T A A A T A A ...

10

20

30

...

MET ASN LYS ILE PHE ASN VAL ILE TRP ASN

...A A T G A A C A A A A T T T T A A C G T T A T T T G G A A

...

40

50

60

V A L V A L T H R G L N T H R T R P V A L V A L S E R ...

T G T T G T G A C T C A A A C T T G G G T T G T C G T A T C ...

70

80

90

...

... G L U L E U T H R A R G T H R H I S T H R L Y S C Y S A L A

...T G A A C T C A C T C G C A C C C A C C A C C A A A T G C G C

...

100

110

120

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S E R A L A T H R V A L A L A V A L A L A L E U A L A ...

C T C C G C C A C C G T G G C A G T T G C C G T A T T G G C ...

130

140

150

...

... T H R L E U S E R A L A T H R V A L G L N A L A A S N

...A A C C C T G T T G T C C G C A A C G G T T C A G G C G A A

...

160

170

180

A L A T H R A S P G L U A S N G L U A S P A S P G L U G L U ...

T G C T A C C G A T G A A A C G A A G A T G A T G A A G A ...

190

200

210

...

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FIG.19B

T G G T A A T T A A G G A A A A

... GLU LEU GLU PRO VAL GIN ARG SER VAL LEU  
...A G A G T T A G A A C C C G T A C A A C G C T C T G T T T  
... 220 230 240

ARG TRP SER PHE LYS SER ALA LYS GLU GLY...  
A A G G T G G A G C T T C A A A T C C G C T A A G G A A G ...  
250 260 270 ...

... THR GLY GLU GIN GLU GLY THR THR GLU VAL  
...C A C T G G A G A C A A G A G G G A A C A C A G A G G T  
... 280 290 300

ILE ASN LEU ASN THR ASP SER SER GLY ASN...  
A A T A A T T T G A A C A C A G A T T C A T C A G G A A A ...  
310 320 330 ...

... ALA VAL GLY SER SER THR ILE THR PHE LYS  
...T G C A G T A G G A A G C A G C A C A A T C A C C T T C A A  
... 340 350 360

ALA GLY ASP ASN LEU LYS ILE LYS GIN SER...  
A G C C G G C G A C A A C C T G A A A A T C A A A C A A G ...  
370 380 390 ...

... GLY ASN ASP PHE THR TYR SER LEU LYS LYS  
...C G G C A A T G A C T T C A C C T A C T C G C T G A A A A  
... 400 410 420

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FIG.19C

GLU LEU LYS ASN LEU THR SER VAL GLU THR...  
AGAGCTGA AAAACCTGACCA GTGTGAAAC...  
430 440 450 ...  
... GLU LYS LEU SER PHE GLY ALA ASN GLY ASN  
...TGAA A A A T T A T C G T T T G G C G C A A C G G C A A  
460 470 480

LYS VAL ASP ILE THR SER ASP ALA ASN GLY...  
TAAAGTTGATATTACCA GTGATGCA AATGG...  
490 500 510 ...  
... LEU LYS LEU ALA LYS THR GLY ASN GLY ASN  
...CTTGAAATTGGCGGAAACACAGGTAA C G G A A A  
520 530 540

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GLY GLN ASN SER ASN VAL HIS LEU ASN GLY...  
TGGTC AAAACAGTAATGTTCACTTAAACGG...  
550 560 570 ...  
... ILE ALA SER THR LEU THR ASP THR LEU ALA  
...TATTGCTTCGACTTTGACCCGATACGCTTGC  
580 590 600

GLY GLY THR THR GLY HIS VAL ASP THR ASN...  
CGGTGGCCACAACAGGACACGTTGACACCAA...  
610 620 630 ...

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FIG. 19D

FIG. 19D

... ILE ASP ALA VAL ASN TYR HIS ARG ALA ALA  
...CATTGATGCGGTTAATTATCATCGCGCTGC  
... 640 650 660

SER VAL GIN ASP VAL LEU ASN SER GLY TRP...  
AAGCGTACAAGATGTGTTAAACAGCGGTTG...  
670 680 690 ...  
... ASN ILE GIN GLY ASN GLY ASN ASN VAL ASP  
...GAATAATCCAGGCAATGGAAACAATGTCTGA  
... 700 710 720

PHE VAL ARG THR TYR ASP THR VAL ASP PHE...  
TTTGTCCGTACTTACGACACCGTGGACTT...  
730 740 750 ...  
... VAL ASN GLY ALA ASN ALA ASN VAL SER VAL  
...TGTC AATGGCGCGCAATGCCCAATGTGAGCGT  
... 760 770 780

THR ALA ASP THR ALA HIS LYS THR THR...  
TACGGCTGATACGGCTCACAAAGACAC...  
790 800 810 ...  
... VAL ARG VAL ASP VAL THR GLY LEU PRO VAL  
...TGTCCTGTGGATGTACAGGCTTGCCGCT  
... 820 830 840

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FIG.19E

GLN TYR VAL THR GLU ASP GLY LYS THR VAL...  
TCAATATGTTACGGGAAGACGGCAAAACCGT...  
850 ... VAL LYS VAL GLY ASN GLU TYR LYS ALA  
...TGTGAAAGTGGGCAATGAGTATTACAAAGC  
880 ... 890 900

LYS ASP ASP GLY SER ALA ASP MET ASN GLN...  
CAAGATGACGGTTTCGGCGGATATGAATCA...  
910 ... LYS VAL GLU ASN GLY LEU ALA LYS THR  
...AAGTCGAAACGGCGAGCTGGCGAAAC  
940 ... 950 960

LYS VAL LYS LEU VAL SER ALA SER GLY THR...  
CAAGTGAAATTGGTATTCGGCAAGCGGTAC...  
970 ... ASN PRO VAL LYS ILE SER ASN VAL ALA ASP  
...AATCCGGTGAAATTAGCAATGTTGCAGA  
1000 ... 1010 1020

GLY THR GLU ASP THR ASP ALA VAL SER PHE...  
CGGCACGGGAAGACACCGGATGCGGTCAAGCTT...  
1030 ... 1040 1050 ...

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FIG.19F

FORGET 299660

... LYS GIN LEU LYS ALA LEU GIN ASP LYS GIN  
...TAAGCAATTAAAGCCCTTGCAAGACAAACA 1080  
... 1060 1070

VAL THR LEU SER THR SER ASN ALA TYR ALA...  
GGTTACGTTGAGCAGCAATGCTTATGC... 1090  
... 1100 1110 ...  
... ASN GLY THR ASP ASN ASP GLY LYS  
...CAATGGCGGTACAGATAACGACGGCGCAA 1140  
... 1120 1130

ALA THR GIN THR LEU SER ASN GLY LEU ASN...  
GGCAACTCAACTTTAAGCAATGGTTTGAA... 1150  
... 1160 1170 ...  
... PHE LYS PHE LYS SER SER ASP GLY LEU  
...TTTAAATTATAATCTAGCGATGGCGAGTT 1200  
... 1180 1190

LEU LYS ILE SER ALA THR GLY ASP THR VAL...  
GTTGAAATAATAGCGCGGACCGGCGATACGGT... 1210  
... 1220 1230 ...  
... THR PHE THR PRO LYS LYS GLY SER VAL GIN  
...TACTTTTACGCCGAAATAAGGTTCCGGTACA 1260  
... 1240 1250

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TTTCTT\*ASPQGGG

FIG.19G

VAL GLY ASP ASP GLY LYS ALA SER ILE SER...  
GTTGGCGATGATGGCAAGGCTTCAATTTC...  
1270 1280 1290 ...  
... LYS GLY ALA ASN THR THR GLU GLY LEU VAL  
...AAGGTGCAATAACAACCTGAAGGTTTGGT  
1300 1310 1320

GLU ALA SER SER GLU LEU VAL GLU SER LEU ASN...  
TAGGCTTCTGAATTGGTTGAAAGCCTGAA...  
1330 1340 1350 ...  
... LYS LEU GLY TRP LYS VAL GLY VAL GLU LYS  
...CAACCTGGGTGGAAAGTAGGGGTTGAGAA  
1360 1370 1380

VAL GLY SER SER GLY GLU LEU ASP GLY THR SER...  
AGTCGGCAGCGCGAGCTTGATGGTACATC...  
1390 1400 1410 ...  
... LYS GLU THR LEU VAL LYS SER GLY ASP LYS  
...CAGGAAACTTTAGTGAAAGTCGGGCGATAA  
1420 1430 1440

VAL THR LEU LYS ALA GLY ASP ASN LEU LYS...  
AGTAACCTTTGAAAGCCGGCGACAATCTGAA...  
1450 1460 1470 ...

FIG. 19H

ALA ASN GLY ALA THR VAL THR ASP ALA ASP...  
 T G C G A A T G G T G C G A C G G T G A C T G A T G C C G A ...  
 1630 1640 1650 ...  
 ... LYS ILE LYS VAL ALA SER ASP GLY ILE SER  
 ... C A G A T T A A G T T G C T T C G G A C G G C A T T A G  
 1660 1670 1680  
 ...



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FIG. 191

FIG.191

ALA GLY ASN LYS ALA VAL LYS ASN VAL ALA...  
CGCGGGTAATAAGCAGTTAAACGTCGC...  
1690 1700 1710 ...  
... ALA GLY GLU ILE SER ALA THR SER THR ASP  
...GGCAGGCCGAAATTTCTGCCACTTCCACCGA  
1720 1730 1740

ALA ILE ASN GLY SER GIN LEU TYR ALA VAL...  
TGGGATTACGGGAAGCCAGTTGTATGCCGT...  
1750 1760 1770 ...  
... ALA LYS GLY VAL THR ASN LEU ALA GLY GIN  
...GGCAAAAGGGGTAAACAACCTTGCTGGACA  
1780 1790 1800

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VAL ASN ASN LEU GLY LYS VAL ASN LYS...  
AGTGAATAATCTTGAGGGCAAGTGAAATAA...  
1810 1820 1830 ...  
... VAL GLY LYS ARG ALA ASP ALA GLY THR ALA  
...AGTGGGCAACGTGCAGATGCAGGTACTGC  
1840 1850 1860

SER ALA LEU ALA ALA SER GIN LEU PRO GIN...  
AGTGCAATAGCGGCTTCACAGTTACCAACA...  
1870 1880 1890 ...

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	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

FIG. 19J

[illegible]

ILE ALA GLY SER SER TYR GLN GLY GLN ASN...  
TAT TGG GGA AGT AGT TAT CAA GGT CAAA ...  
1930 1940 1950 ...

	1960	1970	1980
...	GLY	LEU	ALA
...	ILE	GLY	VAL
...	SER	ARG	ILE
...	SER	ARG	ILE
...	TTT	CTA	TCA
...	AGT	GGA	AGT
...	TTC	TTC	TTC

ASP ASN GLY LYS VAL ILE ILE ARG LEU SER...  
CGATAATGGCAAAGTGATTAATTCGCTTGTCTC...  
1990 2000 2010 ...

... GLY THR THR ASN SER GLN GLY LYS THR GLY  
 ...AGGCACAACCAATAGTC AAGGTAACAACAGG 2020 2030 2040

VAL ALA ALA GLY VAL GLY TYR GLN TRP \*\*\*  
CGT TGC AGC A GGT GTT GGT TACC AGT GGT A...

...ATAGAATTC

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FIG. 20A

FIG. 20A

NIHi strain 29 Hia

TTAAATATAAGGTAAATAAATAAGAACAA...  
10 20 30...  
... ILE PHE ASN VAL ILE TRP ASN VAL VAL THR  
... ATTTTAAACGTTATTGGAATGTTGTGACT  
40 50 60

GLN THR TRP VAL VAL VAL SER GLU LEU THR ...  
CAAACTTGGGTTGTCGTATCTGAACCTCACT...  
70 80 90...  
... ARG ALA HIS THR LYS CYS ALA SER ALA THR  
... CGCGCCCAACCAAAATGCGCCTCCGCCACC  
100 110 120

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VAL ALA VAL ALA VAL LEU ALA THR ALA LEU ...  
GTGGCGGTTGCGCGTATTGGCAACTGCGTTG...  
130 140 150...  
... SER ALA THR ALA GLU ALA ASN ASN THR  
... TCTGCAACGGCTGAAGCGGAACAATACT  
160 170 180

SER VAL THR ASN GLY LEU ASN ALA TYR GLY ...  
TCTGTACGAATGGGTTGAATGCTTATGGC...  
190 200 210...

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SEQUENCE

FIG.20B

... ASP THR ASN PHE ASN THR THR ASN ASN SER  
... GATACATAATTATAATACCAATAATTCCG 240  
... 220 230

ILE ALA ASP LEU GLY LYS HIS VAL GLN ASP ...  
ATAGCAGATTGTGAAACACGTTCAAGAT... 260  
... 250 270...  
... ALA TYR LYS GLY LEU LEU ASN LEU ASN GLU  
... GCTTATAAAGGCTTATTAAATCTGAATGAA 300  
... 280 290

LYS ASP THR ASN LYS SER PHE LEU VAL ...  
AAGATACAAATAAGTCAAGTTCTTGTT... 310  
... 320 330...  
... ALA ASP ASN THR ALA ALA THR VAL GLY ASN  
... GCCGACAATACCGCCGCAACCGTAGGCAAT 360  
... 340 350

LEU ARG LYS LEU GLY TRP VAL LEU SER ...  
TTGCGTAATAATTGGGCTGGGTATTGTCTAGC... 370  
... 380 390...  
... LYS ASN GLY THR ARG ASN GLU LYS SER TYR  
... AAAACGGCACAAAGGAACGAGAAAGCTAT 420  
... 400 410

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FIG. 20C

FIG. 20C

GLN VAL LYS LYS GLN ALA ASP GLU VAL LEU PHE ...  
CAAGTAAACAAGCTGATGAAGTTCTCTT...  
430 440 450...

... THR GLY SER GLY ALA THR VAL SER SER  
... ACTGGATCTGGTGCTGCAACGGTTAGTTCC  
460 470 480

SER SER LYS LYS ASP GLY LYS HIS THR ILE THR ...  
AGCTCTAAAGACGGTAACAATACCATTAAC...  
490 500 510...

... ILE SER VAL THR LYS GLY SER PHE ALA GLU  
... ATTCTGTACCAAGGTAGTTTGTCTGAG  
520 530 540

VAL LYS THR ASP ALA THR GLY GLN ...  
GTAAACTGATGCACCTACTGGAGGTCAA...  
550 560 570...

... VAL ASN ALA ASP ARG GLY LYS VAL LYS ALA  
... GTAAACGCCGACCGTGGTAAAGTGAAAGCT  
580 590 600

GLU ASP GLU ASN GLY ALA ASP VAL ASP LYS ...  
GAGGACGAGAAATGGAGCTGATGTTGATAAG...  
610 620 630...

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FIG. 20D

FIG. 20D

... LYS VAL ALA THR VAL LYS ASP VAL ALA LYS  
... AAAGTTGCCAACTGTAAAGATGTTGCTAAG 660  
... 640 650

ALA ILE ASN ASP ALA ALA THR PHE VAL LYS ...  
GCGATTAAACGATGCCCGCAACTTTCGTGAA... 670  
... VAL GLU SER THR ASP ASP ILE GLU ASN  
... GTGGAAAGCACAGATGATGACATTGAAAT 720  
... 690... 710

GLY ALA ALA GLY LYS ASN GLU THR THR ASP ...  
GGTGCTGCAGGCAAAATGAACTACAGAC... 730  
... GLN ALA LEU LYS ALA GLY ASP THR LEU THR  
... CAAGCTCTCAAGCAGCGGACACCTTAACC 780  
... 740 750... 760 770

LEU LYS ALA GLY LYS ASN LEU LYS ALA LYS ...  
TTAAAGCGGGTAAACCTTAAGCTAAG... 790  
... LEU ASP GLN ASN GLY LYS SER VAL THR PHE  
... TTAGACCAAAATGGTAAATCAGTAACCTTT 840  
... 800 810... 820 830 840

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115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

FIG.20E

ALA LEU ALA LYS ASP LEU ASP VAL THR SER ...  
GCTTAGCGGAAAGACCTTGATGTGACCTCT... 860  
... ALA LYS VAL SER ASP LYS LEU SER ILE GLY 870...  
... GCGAAAGTGAGTGATAGTTGTCTATTGGT 880  
... 890  
... 900

LYS ASP THR ASN LYS VAL ASP ILE THR SER ...  
AAGATACGAAATAAAGTTGATATTACCACT... 910  
... ASP ALA ASN GLY LEU LYS LEU ALA LYS THR 920  
... GATGCAAAATGGCTTGAAATTGGCGAAACA 930...  
... 940  
... 950  
... 960

GLY ASN GLY ASN GLY GLN ASN GLY ASN VAL ...  
GGTAACGGAAATGGTCAAAACGGTAATGTC... 970  
... HIS LEU ASN GLY ILE ALA SER THR LEU THR 980  
... CACTTAAATGGTATTGCTTCGACTTTGACC 990  
... 1000  
... 1010  
... 1020

ASP THR ILE THR GLY MET THR THR GLN ALA ...  
GATACCATTACAGGTATGACACACACAGCA... 1030  
... 1040  
... 1050...

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FIG.20F

TTTTTTT TTTT

... SER ASN GLY VAL ALA VAL GIN ASN HIS ASN 1080  
... AGCAATGGCGTGGCTGTGCAGAAATCATAT 1070  
... 1060

ARG ALA ALA SER VAL ALA ASP VAL LEU ASN ...  
CGTGCTGCGAGTGTGGCTGATGTTAAT... 1100  
... ALA GLY TRP ASN ILE GIN GLY ASN GLY ALA 1140  
... GCAGGCTGGAAATATTCAAGGCCAACGGAGCG 1130  
... 1120

SER VAL ASP PHE VAL ASN ALA TYR ASP THR ...  
AGCGTTGATTTTGTCAATGCTTACGACACA... 1160  
... VAL ASP PHE VAL ASN GLY THR ASN THR ASN 1200  
... GTAGATTTTGTCAATGGTACAAACACCAAT 1190  
... 1180

VAL ASN VAL THR THR ASP THR ALA HIS LYS ...  
GTGAACGTTACGACTGATACGGCTCACAA... 1210  
... LYS THR THR VAL ARG VAL ASP VAL THR GLY 1260  
... AAGACAACCGTCCGTGTGGTGTACAGGC 1250  
... 1240



FIG. 20G

FIG. 20G

LEU PRO VAL GLN TYR VAL THR GLU ASP GLY ...  
TTGCCGGTTTCAATATGTTACGGGAAGACGGC...  
1270 1280 1290...  
... LYS THR VAL VAL LYS VAL ASP ASN LYS TYR  
... AAAACCGTTGTGAAGTGGACAAATAAGTAT  
1300 1310 1320

TYR GLU ALA LYS GLN ASP GLY SER ALA ASP ...  
TACGAAGCTAAGCAAGACGGTTTCGGCGGAT...  
1330 1340 1350...  
... MET ASP LYS LYS VAL GLU ASN GLY LEU  
... ATGGATAAATAAGTCCGAATAATGGCGAGCTG  
1360 1370 1380

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ALA LYS THR LYS VAL LYS LEU VAL SER ALA ...  
GCGAAACCAAGTGAAATTGGTGTTCGGCA...  
1390 1400 1410...  
... SER GLY GLN ASN PRO VAL LYS ILE SER ASN  
... AGCGGTCAAAATCCGGTGAAATCAGCAAT  
1420 1430 1440

VAL ALA GLU GLY THR GLU GLU ASN ASP ALA ...  
GTTGCGGAAGGCAAGGGAAGAAACGATGCG...  
1450 1460 1470...

FIG. 20H

... ASP THR VAL THR PHE THR PRO LYS LYS GLY  
... GACACAGTTACCTTTACGCCGAAAAAAGGT

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TTTATT" 29E9E660

FIG.20I

SER VAL GLN VAL GLY GLU ASP GLY LYS ALA ...  
TCGGTACAGGTTGGCGAAGACGGTAAGGCT...  
1690 1700 1710...  
... THR ILE GLN ASN GLY THR LYS THR ASP  
... ACGATTCAAAATGGGTACGAAACCAACCGAC  
1720 1730 1740  
...

GLY LEU VAL GLU ALA SER GLU LEU VAL GLU ...  
GGTTTGGTTGAAGCTTCCGAAATTGGTTGA...  
1750 1760 1770...  
... SER LEU ASN LYS LEU GLY TRP LYS VAL GLY  
... AGCCTGAACAACCTGGGCTGGAAAGTGGGC  
1780 1790 1800  
...

VAL ASP LYS ASP GLY SER GLY GLU LEU ASP ...  
GTTGATAAAGACGGCAGCGCGAGCTTGAT...  
1810 1820 1830...  
... GLY ALA SER ASN GLU THR LEU VAL LYS SER  
... GGTGCATCCAAATGAACTTTAGTGAGTCCG  
1840 1850 1860  
...

GLY ASP LYS VAL THR LEU LYS ALA GLY GLU ...  
GGCGATAAAGTAACCTTTGAAAGCCGGCGAG...  
1870 1880 1890...  
...

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FIG.20J

TTCTCTT 2222222222

... ASN LEU LYS VAL LYS GIN ASP GLY THR ASN  
... AATCTGAAGGTCAACAACAGACGGCACAAAC  
... 1900 1910 1920

PHE THR TYR ALA LEU LYS ASP GLU LEU THR ...  
TTCACTTACGGCTCAAGAATGATGACG...  
1930 1940 1950...  
... GLY VAL LYS SER VAL GLU PHE LYS ASP THR  
... GGCGTGAAAGAGCGTGAGTTTAAAGACACG  
... 1960 1970 1980

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ALA ASN GLY SER ASN GLY ALA SER THR LYS ...  
GCGAATGGTTCAACGGGTGCAAGCACGAAG...  
1990 2000 2010...  
... ILE THR LYS ASP GLY LEU THR ILE THR SER  
... ATTACCAAGACGGCTTGACCATTACGTCG  
... 2020 2030 2040

ALA ASN GLY ALA ASN GLY ALA ALA THR ...  
GCAACGGTGCGAATGGTGCGGCGGCGACT...  
2050 2060 2070...  
... ASP ALA ASP LYS ILE LYS VAL ALA SER ASP  
... GATGCGGACAAAGATTAAAGTGGCTTCAGAC  
... 2080 2090 2100

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FIG.20K

11/11/2000 20:00:00

GLY ILE SER ALA GLY ASN LYS ALA VAL LYS ...  
GGCATCAGTGGCGGTTAATAAGCGGTTAA...  
2110 2120 2130...  
... ASN VAL VAL SER GLY LYS LYS PHE GLY  
... AACGTTGTGAGCGGACTGAAGAAATTGGT  
... 2140 2150 2160

ASP ALA ASN PHE ASN PRO LEU THR SER SER ...  
GATGCCGAATTTCATAATCCACTGACCAGTTCC...  
2170 2180 2190...  
... ALA ASP ASN LEU THR LYS GLN TYR ASP ASP  
... GCCGACAACCTTAACGAAACAATAATGACGAT  
... 2200 2210 2220

ALA TYR LYS GLY LEU THR ASN LEU ASP GLU ...  
GCCCTATAAGGCTTGACCAATTGGATGA...  
2230 2240 2250...  
... LYS GLY ALA ASP LYS GLN THR LEU THR VAL  
... AAAGGTGGGACCAAGCAAACTCTGACTGTT  
... 2260 2270 2280

ALA ASP ASN THR ALA THR VAL GLY ASP ...  
GCCGACAATACTGCCGCCAACCGTGGGCGAT...  
2290 2300 2310...

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SEQUENCE

FIG.20L

... LEU ARG GLY LEU GLY TRP VAL ILE SER ALA  
... TTGGCGGCTTGGGCTGGGTCATTCTGCG 2340  
... 2320

ASP LYS THR THR GLY GLU LEU ASN LYS GLU ...  
GACAAACACAGGCGA ACTCAATAAGGA... 2350  
... 2360  
... TYR ASN ALA GLN VAL ARG ASN ALA ASN GLU  
... TACAACGCGCAAGTGCGTAACGCCAATGAA 2400  
... 2380

VAL LYS PHE LYS SER GLY ASN GLY ILE HIS ...  
GTGAATAATTCAGAGCGGCAACGGTATCCAT... 2410  
... 2420  
... VAL SER GLY LYS THR VAL ASN GLY ARG  
... GTTTCGGGTAAACGGTCAACGGTAGGCGC 2460  
... 2440

GLU ILE THR PHE GLU LEU ALA LYS ASP GLU ...  
GAAATTA CTTTGTGAATTGGCTAAAGACGA... 2470  
... 2490  
... ASN ALA ILE ALA PHE GLY TYR GLY SER LYS  
... AATGCCATTGCTTTCGGTTATGGCTCAAAA 2520  
... 2500

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TYR LYS ALA ASN GLY ASP VAL ASP THR GLU ...  
 TATAAGCCAA TGGAGATGTGATACGGA A...  
 2710 2720 2730...

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FIG.20N

THESE ARE THE SEQUENCES

... THR VAL THR VAL LYS ASP LYS ASP GLY LYS  
... ACCGTAAACCGTTAAGGACAAAGACGGTAAA 2760  
... 2740 2750

GLU THR THR VAL THR VAL PRO LYS ALA LEU ...  
GAGACTACCGTTACTGTTCCTAAAGCGTTA... 2780  
... 2790...  
... GLY ALA THR VAL GLU ASN SER VAL TYR LEU  
... GGGGCTACGGTTGAAACCTCCGTTATTG 2820  
... 2800 2810

GLY ASN LYS SER THR ALA THR LYS ASP LYS ...  
GGTAATAAATCGACTGCGACAAAGATAAG... 2840  
... 2850...  
... GLY LYS ASN LEU LYS SER ASP GLY THR ALA  
... GGTAATAAACCTGAATCTGATGGTACGGCG 2880  
... 2860 2870

GLY ASN THR THR THR ALA GLY THR GLY ...  
GGTAACACTACAACCTGCTGGCACACGGGT... 2890  
... 2910...  
... THR VAL ASN GLY PHE ALA GLY ALA THR ALA  
... ACGGTAAACGGCTTTGCCGGGTGCAACGGCG 2940  
... 2920 2930



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FIG.200

HIS GLY ALA VAL SER VAL GLY ALA SER GLY ...  
C A C G G T G C G G T T T C T G T C G G C G C A A G C G G C ...  
2950  
2960  
... GLU GLU ARG ARG ILE GLN ASN VAL ALA ALA  
... G A G A A A G A C G T A T C C A A A C G T C G C G G C A  
2980 2990 3000

GLY GLU ILE SER ALA THR SER THR ASP ALA ...  
G G C G A A A T T T C C G C C A C T T C C A C C G A T G C G ...  
3010 3020 3030 ...  
... ILE ASN GLY SER GLN LEU TYR ALA VAL ALA  
... A T T A C G G C A G C C A G T T G T A T G C T G T G G C A  
3040 3050 3060

LYS GLY VAL THR ASN LEU ALA GLY GLN VAL ...  
A A G G G G T A A C A A A T C T T G C T G G A C A A G T G ...  
3070 3080 3090 ...  
... ASN LYS VAL GLY LYS ARG ALA ASP ALA GLY  
... A A T A A A G T G G G C A A C G T G C A G A T G C A G G T  
3100 3110 3120

THR ALA SER ALA LEU ALA ALA SER GLN LEU ...  
A C A G C A A G T G C A T T A G C A G C T T C A C A G T T A ...  
3130 3140 3150 ...

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TABLE PREPARED

FIG.20P

... PRO GLN ALA SER MET PRO GLY LYS SER MET  
... CCACAAGCCTCTATGCCAGGTAATCAATG 3180  
... 3160 3170

VAL SER ILE ALA GLY SER TYR GLN GLY ...  
GTTTCTATTGCGGGAAGTAGTTATCAAGGT... 3200  
... 3190 3210...  
... GLN ASN GLY LEU ALA ILE GLY VAL SER ARG  
... CAAATGGTTTAGCTATCGGGGTATCACGA 3240  
... 3220 3230

ILE SER ASP ASN GLY LYS VAL ILE ILE ARG ...  
ATTCCGATAATGGCAAGTGATTATTCGC... 3260  
... 3250 3270...  
... LEU SER GLY THR THR ASN SER GLN GLY LYS  
... TTGTCAGGCACAACCAATAGCCAGGTAATA 3300  
... 3280 3290 3300

THR GLY VAL ALA GLY VAL GLY TYR GLN ...  
ACAGGCGTTGCAGCAGGTTGTTGTTACCAG... 3310  
... 3320 3330...  
... TRP \*\*\*  
... TGGTAATAGAAATCCGGATCCGC 3350  
... 3340

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[illegible]

FIG. 21A

NTHi strain M4071 Hia

MET ASN LYS ILE PHE ASN VAL...  
 GCGAATTCAATGAAACAATTTTTAACGT...  
 10 20 30 ...  
 ... ILE TRP ASN VAL MET THR GLN THR TRP ALA  
 ...TATTGGAAATGTTATGACTCAACCTGGGC  
 40 50 60

[illegible][illegible]

THR	ASN	GLY	LEU	LYS	ALA	TYR	GLY	SER	THR...
TACAAACGGGTTTGAAAGCCTTATGGAGGTAC...	190				200			210 ...	

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FIG. 21B

FIG. 21B

... ASN ASN PRO ASN PHE ASN ALA ALA GLY ASN  
...GAATAATCCGAATTTC AATGCTGCAGGTAA 240  
... 220 230

SER ALA THR ASP LEU ALA ARG GIN PHE ASP...  
CTCTGCAACTGATTAGCTAGACAGTTTGA... 260  
... 270 ...

... GLY ALA TYR ASP GLY LEU LEU ASN LEU ASN  
...TGGTGCTTATGACGGTTTATTAAATCTAAA 300  
... 280 290

GLU LYS ASP ALA ASN LYS ASN LEU VAL...  
TGAAAAGATGCGGAATAAATCTGTGTT... 320  
... 310 330 ...

... THR ASP ASP LYS ALA ALA THR VAL GLY ASN  
...GACTGATGATAAGCGCGGACCGTAGGCAA 360  
... 340 350

LEU ARG LYS LEU LEU GLY TRP VAL LEU SER...  
TTTGGCTAAATTGGGTTGGGTATTGTCTAG... 380  
... 370 390 ...

... LYS ASN GLY THR ARG ASN GLU LYS SER GIN  
...TAAACGGGCACAGGACGAGAAAGCCA 420  
... 400 410

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FIG.21C

GLN VAL LYS HIS ALA ASP GLU VAL LEU PHE...  
ACAACTCAAAACACCGGATGAAGTTGTT...  
430  
... GLU GLY LYS ASP GLY VAL THR VAL THR SER  
...TGAAGGCAAGACGGTGTAACGGTTACTTC  
440 450 ...  
460 470 480

LYS SER GLU ASN GLY LYS HIS THR VAL THR...  
CAAACTCGAAACCGGTAAACACCGTTAC...  
490 500 510 ...  
... PHE THR LEU GLU LYS ASP LEU ASN VAL LYS  
...TTTACCCTTGAGAAAGACCCTTAATGTAAA  
520 530 540

ASN ALA THR VAL SER ASP LYS LEU SER LEU...  
AAACGCAACCGTTAGCGATAAATTATCGCT...  
550 560 570 ...  
... GLY ALA ASN GLY ASN LYS VAL ASP ILE THR  
...TGGTGCAACCGGCAATAAAGTCGATATTAC  
580 590 600

SER ASP THR ASN GLY LEU LYS PHE ALA LYS...  
CAGTGATACAAACCGGCTTGAAATTGCGAA...  
610 620

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FIG.21D

... PRO SER THR ASN GLY GIN ASN GLY ASN VAL  
... ACCAAGTACGAATGGTCAAAACGGTAATGT 660  
... 640 650

HIS LEU ASN GLY ILE ALA SER THR LEU THR...  
TCACTTAACCGGTATTGGCCCTCTACCTTAAC... 670  
... 680 690 ...

... ASP THR ILE THR GLY THR THR LYS SER ALA  
... TGACACAAATTACAGGTACAAACAATACTCTGC 720  
... 700 710

THR ASN GLY VAL ASP VAL GIN ASN HIS ASN...  
AACTAATGGTGTAGATGTGCAGAAATCAATA... 730  
... 740 750 ...

... ARG ALA ALA SER VAL ALA ASP VAL LEU ASN  
... TCGTGCTGCGAGTGTAGCTGATGTATTGAA 780  
... 760 770

ALA GLY TRP ASN ILE GIN GLY ASN GLY ALA...  
TGCAGGCTGGGAATATTCAAGGCAACGGAGC... 790  
... 800 810 ...

... SER VAL ASP PHE VAL ASN THR THR ASP THR  
... GAGCGTTGATTTTGTCAATACTTACGACAC 840  
... 820 830

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FIG.21E

VAL ASP PHE VAL ASN GLY LEU ASN THR ASN...  
AGTAGATT TTTGTC AATGGTTTAAATACCAA...  
850 860 870 ...  
... VAL ASN VAL THR THR ASP THR ALA HIS ASN  
...TGTGAACGTTACGACTGATACGGCTCACAA  
880 890 900

LYS LYS THR THR VAL ARG VAL ASP VAL THR...  
CAAAAGACAACCGTCCGTGTTGGAATGTAAAC...  
910 920 930 ...  
... GLY LEU PRO VAL GIN TYR VAL THR GLU ASP  
...GGGCTTGCCGGTCCCAATATGTTACGGAGA  
940 950 960

GLY GLU THR THR VAL VAL LYS VAL GLY ASN GLU...  
CGGCCGAAACCGTTGTGAAGTGGGCAATGA...  
970 980 990 ...  
... TYR TYR GLU ALA LYS GIN ASP GLY SER ALA  
...GTATTACGAAGCCCAAGCAAGACGGTTCCGGC  
1000 1010 1020

ASP MET ASP LYS LYS VAL GLU ASN GLY LYS...  
GGATATGGATAAAGTTCGAAATGGCAA...  
1030 1040 1050 ...

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FIG. 21F

FIG. 21F

... LEU ALA LYS THR LYS VAL LYS LEU VAL SER  
...GCTGGCGAAACTAAAGTTAAATTGGTATC 1080  
... 1060 1070

ALA ASN GLY THR ASN PRO VAL LYS ILE SER...  
GGCAACCGGTACAAATCCGGGTGAAATCAG ... 1100  
... ASN VAL ALA ASP GLY THR GLU ASN THR ASP  
...CAATGTTGCGGACGGCACCGGAAATACCGA 1140  
... 1120 1130

ALA VAL SER PHE LYS GLN LEU LYS ALA LEU...  
TGGGTCAGCTTTAAGCAGTTGAAGCCTT ... 1160  
... GIN ASP LYS GLN VAL THR LEU SER ALA SER  
...GCAAGACAAACAGGTTACGTTAAGTGCGAG 1200  
... 1180 1190

ASN ALA TYR ALA ASN GLY GLY SER ASP ALA...  
CAATGCTTATGCCCAATGGCGGTAGCGATGC ... 1230  
... ASP GLY GLY LYS GLY ILE GIN THR LEU SER  
...CGACGGCGGCAAGGGAATTCAACTTTAAG 1260  
... 1240 1250



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FIG.21G

ASN GLY LEU ASN PHE LYS SER THR...  
CAATGGTTTGAAATTTAAATTTAAATCCAC...  
1270 1280 1290 ...  
... ASP GLY GLU LEU LEU ASN ILE LYS ALA GLU  
...AGACGGCGAGTTGTTGAATATCAAAAGCAGA  
1300 1310 1320

ASN ASP THR VAL THR PHE THR PRO LYS LYS...  
AAATGACACGGTTTACCTTTACGCCGAA...  
1330 1340 1350 ...  
... GLY SER VAL GLN VAL GLY ASP GLY LYS  
...AGGTTTCGGTGCAAGTTGGCGATGATGGTAA  
1360 1370 1380

ALA THR ILE GIN ASP GLY ALA LYS THR THR...  
GGCTACGATTCAAGACGGCGCAAAACAAC...  
1390 1400 1410 ...  
... THR GLY LEU VAL GLU ALA SER GLU LEU VAL  
...TACCGGTTTGGTTGAGGCTTCTGAATTGGT  
1420 1430 1440

ASP SER LEU ASN LYS LEU GLY TRP LYS VAL...  
TGACAGCCCTGAACAATAATGGGTTGGAAAGT...  
1450 1460 1470 ...

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FIG.21H

... GLY THR GLY THR ASP GLY THR GLY VAL THR  
...GGGCACCGGCACTGACGGCACAGGAGTGAC 1500  
... 1480 1490

ASP GLY THR THR HIS THR ASP THR LEU VAL LYS...  
CGATGGCACGCATACCGACACTTTAGTGAA... 1510  
... 1520 1530 ...

... SER GLY ASP LYS VAL THR LEU LYS ALA GLY  
...GTCGGGCGATAAAGTAACCTTTGAAAGCCGG 1550  
... 1540 1560

ASP ASN LEU LYS VAL LYS GLN GLU GLY THR...  
CGACAATCTGAAGGTCAACACAGAGGGTAC... 1570  
... 1580 1590 ...

... ASN PHE THR TYR ALA LEU LYS ASP GLU LEU  
...AAACTTCACTTATGCGCTCAAGATGAATT 1610  
... 1600 1620

THR ASP VAL LYS SER VAL GLU PHE LYS ASP...  
GACGGACGTGAAGAGCGGTGGAGTTTAAAGA... 1630  
... 1640 1650 ...

... THR ALA ASN GLY ALA ASN GLY ALA SER THR  
...CACGGCGAATGGTGCAACCGGTGCAAGCAC 1670  
... 1660 1680

TCGTTAT-29C9E55D

FIG.21I

LYS ILE THR LYS ASP GLY LEU THR ILE THR...  
GAAGATTACCAAGAGACGGCTTGACCATTAC...  
1690 1700 1710 ...  
... PRO ALA ASN GLY ALA GLY ALA ALA GLY ALA  
...GCCGGCAACGGTGCGGGTGCGGGCAGGTGC  
1720 1730 1740

ASN THR ALA ASN THR ILE SER VAL THR LYS...  
AAACACTGCAACACCAATTAGCGTAACCAA...  
1750 1760 1770 ...  
... ASP GLY ILE SER ALA GLY ASN LYS ALA VAL  
...AGACGGCATTAGCGGGGTATAAAGCAGT  
1780 1790 1800

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LYS ASN VAL VAL SER GLY LEU LYS LYS PHE...  
TAAACGTTGTGAGCGGACTGAAGAAAT...  
1810 1820 1830 ...  
... GLY ASP ALA ASN PHE ASP PRO LEU THR SER  
...TGGTGATGCCGAATTTCGATCCGCTGACTAG  
1840 1850 1860

SER ALA ASP ASN LEU THR LYS GLN TYR ASP...  
CTAGCCGACAACTTAACGAACAATAATGA...  
1870 1880 1890 ...

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FIG.21J

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... ASN ALA TYR LYS GLY LEU THR ASN LEU ASP  
...CAATGCCCTATAAAGGCTTGACCAATCTGGA 1920  
... 1900

GLU LYS SER LYS GLY LYS GLN THR PRO THR...  
TGAAAAGTAAAGGCAAGCAACTCCGAC... 1940  
... VAL ALA ASP ASN THR ALA ALA THR VAL GLY  
...CGTTGCTGACAAATACCGCTGCAACCGTGGG 1980  
... 1960

ASP LEU ARG ARG GLY LEU GLY TRP VAL ILE SER...  
CGATTTCGCGCGGCTTGCGCTGGGTCTTTC... 2000  
... ALA ASP LYS THR LYS GLY GLU LEU ASN LYS  
...TGCAAGACAAACCAAGGCGGAATCAATAA 2040  
... 2020

GLU TYR ASN ALA GIN VAL ARG ASN ALA ASN...  
GGAATACACGCAAGTGGCTAACGCTAA... 2060  
... GLU VAL LYS PHE LYS SER GLY ASN GLY ILE  
...TGAAAGTGAATTCAGAGCGGCAACGGTAT 2100  
... 2080

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FIG. 21K

FIG.21K

ASN VAL SER GLY LYS THR LEU ASP ASN GLY...  
CAATGTTTCCGGTAACAATTTGGATAACGG...  
2110 2130 ...  
... THR ARG GLU ILE THR PHE GLU LEU ALA LYS  
...TACGGCGCGAAATTACTTTTGAATTGGCTAA  
2140 2150 2160

ASP GLU ASN ALA ILE ALA PHE GLY SER GLY...  
AGACGAAATAAGCCATTGCTTTTCGGTTCTGG...  
2170 2190 ...  
... SER LYS ALA LEU ARG ASP ASN THR VAL ALA  
...CTCAAAAGCCCTTGCGCGGATAACACGGTGGC  
2200 2210 2220

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ILE GLY THR GLY ASN VAL VAL ASN ALA GLU...  
AATTGGTACGGGCAACGTTGTGAAATGCGGA...  
2230 2250 ...  
... LYS SER GLY ALA PHE GLY ASP PRO ASN TYR  
...AAAATCTGGTGCAATTCGGCGGATCCGAACTA  
2260 2270 2280

ILE GLU ASP LYS ALA GLY GLY SER TYR ALA...  
CATCGAAGATAAAGCCGGTGGCAGCTACGC...  
2290 2310 ...

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SEQUENCE

FIG.21L

... PHE GLY ASN ASP ASN ARG ILE THR SER LYS  
...TTTCGGTAACGATAACCGTATTACTTCTAA 2340  
... 2320 2330

ASN THR PHE VAL LEU GLY ASN SER VAL ASN...  
AAACACTTTTGTGTTGGTAATAGTTTAA... 2350  
... 2360 2370 ...  
... ALA LYS ARG ASP ALA ASN GLY ASN VAL LEU  
...TCCGAAACGTGATGCATAATGGCAATGTACT 2400  
... 2380 2390

THR GLU GLU LYS GLU VAL VAL GLY LYS ASP...  
GACCGAAGAAAGAGAGTGGTTGGAAAGA... 2410  
... 2420 2430 ...  
... GLY ALA LYS THR LYS VAL THR VAL PRO GLN  
...CGGTGCGAAGACGAAAGTAACCGTGCCGCA 2460  
... 2440 2450

ALA LEU GLY GLU THR VAL GLU ASN SER VAL...  
AGCCTTAGGCGAAGAACCGTAGAAATTCTGT... 2470  
... 2480 2490 ...  
... TYR LEU GLY ASN ALA SER THR ALA THR LYS  
...TTATCTCCGGTAATGCTTCACTGCCGACAA 2520  
... 2500 2510

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FIG.21M

ASP LYS GLY LYS ASN LEU LYS SER ASP GLY...  
AGATAAGGGTAAATAACCTGAAATCTGATGG...  
2530 2540 2550 ...  
... THR ALA GLY ASN THR THR THR ALA GLY ALA  
...TACGGCGGTAACTACTACAACTGCTGGCGC  
2560 2570 2580

THR GLY THR VAL ASN GLY PHE ALA GLY ALA...  
AACGGGTACGGTAAACGGCTTTGGCGGTGC...  
2590 2600 2610 ...  
... THR ALA HIS GLY ALA VAL SER VAL GLY ALA  
...AACGGCGCACGGTGCGGTTTCTGTCGGCGC  
2620 2630 2640

SER GLY GLU GLU ARG ARG ILE GLN ASN VAL...  
AGTGGCGAAGAAAGACGTATCCAAACGT...  
2650 2660 2670 ...  
... ALA ALA GLY GLU ILE SER ALA THR SER THR  
...CGCGGCAGCGGAATTTCCTTCTTCCCTACTTCCAC  
2680 2690 2700

ASP ALA ILE ASN GLY SER GLN LEU TYR ALA...  
AGATGCCGATTAAACGGGTAGCCAGTTGTATGCC...  
2710 2720 2730 ...

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FIG. 21N

FIG. 21N

... VAL ALA LYS GLY VAL THR ASN LEU ALA GLY  
...TGTGGCAAAAGGGGTAACAAACCTTGCTGG 2760  
... 2740 2750

GLN VAL ASN LYS VAL GLY LYS ARG ALA ASP...  
ACAAGTGAAATAAAGTGGGCAAAACGTGCAGA... 2770  
... 2780 2790 ...

... ALA GLY THR ALA SER ALA LEU ALA ALA SER  
...TGCAGGTACAGCAAGTGCAATTAGCGGCTTC 2800  
... 2810 2820

GLN LEU PRO GIN ALA SER MET PRO GLY LYS...  
ACAGTTACCAACAAGCCCTCTATGCCAGGTAA... 2830  
... 2840 2850 ...

... SER MET VAL SER ILE ALA GLY SER SER TYR  
...ATCAATGGTTTCTATTGCGGGAAGTAGTTA 2860  
... 2870 2880

GLN GLY GIN SER GLY LEU ALA ILE GLY VAL...  
TCAAGGTCAAAAGTGGTTTAGCTATCGGGT... 2890  
... 2900 2910 ...

... SER ARG ILE SER ASP ASN GLY LYS VAL ILE  
...ATCAAGAAATTTCCGATAATGGCAAGTAGT 2920  
... 2930 2940



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FIG. 210

FIG.210

ILE ARG LEU SER GLY THR THR ASN SER GLN...  
TATTCGCTTGTTCAGGCACACCAATAGCCA...  
2950 2960 2970 ...

... GLY LYS THR GLY VAL ALA ALA GLY VAL GLY  
...AGGTAAACAGGCCGTTGCAGCAGGTGTTGG  
2980 2990 3000

TYR GLN TRP \*\*\* \*\* ASN SER GLY SER  
TTACCAAGTGGTAATAGAAATTCCTGGATCCGC  
3010 3020 3030

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FIG. 22A

### NTHi strain K9 hia sequence

MET	ASN	LYS	ILE	PHE	ASN	VAL	ILE	TRP	ASN ...
A	T	G	A	C	A	A	A	T	T T A C G T A T T T G G A A T . . .
10									
... VAL MET THR GLN TRP ALA VAL SER	20 : 30...								
... GTT ATG ACT CAAC TGG GCCTGT CGTA CTCT									
...	40							50	60

GLU	LEU	THR	ARG	ALA	HIS	THR	LYS	ARG	ALA ...
G A C T C A C T C G C G C C C A C A C C A A C G T G C C . . .									
									70
									80
							SER	ALA	THR VAL ALA THR ALA VAL LEU ALA
							. . .		
							T C C G C A A C C G T G G C G A C C G C C G T A T T G G C G		
							. . .		90... 100 110 120

THR GIN LEU SER ALA THR ALA GLU ALA ASN ...  
 ACGCAGTTGTC TGCACGGCTGAGCGAAC...  
 130 140 150...  
 ... SER SER ALA SER VAL THR SER ARG LEU ASN  
 ... AGTAGTGCTTCTGTTACGAGTAGGTGAAT  
 ... 160 170 180

VAL TYR GLY ASP THR ASN THR LYS PHE ASN ...  
GTTATGGCGATACGAATACATAAATCAAT...  
190 200 210...

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FIG. 22B

FIG. 22B

... ALA ALA ASN SER ILE ALA ASP LEU ASN  
... GCAGCCAATAATTCAATAGCAGATTTAAT 240  
... 220 230

LYS GLN ASN ASP GLY VAL HIS ASP GLY LEU ...  
AAACAATAATGATGGTGTTCACGATGGTTTA... 250  
... 260 270...  
... LEU ASN LEU ASN GLU ASN GLY ALA ASN LYS  
... TAAATCTGAATGAATAACGGTGCGAATAAA 300  
... 280

LYS LEU VAL ASP ASP THR ALA ...  
AAGCTGTTGGTGGATGACAAATACTGGCGCG... 310  
... 320 330...  
... THR VAL GLY ASP LEU ARG LYS LEU GLY TRP  
... ACCGTAGGCGATTACGTAAATTGGGCTGG 360  
... 340 350

VAL VAL SER THR LYS ASN GLY LYS GLU ASN ...  
GTCGTATCAACCAAAATGGCAAGGAAAT... 370  
... 380 390...  
... GLU LYS SER GLN VAL LYS GLN ALA ASP  
... GAGAAAGCCCAACAAGTCAACAGCGGAT 420  
... 400 410

TABLET 2999660

FIG.22C

GLU VAL LEU PHE LYS GLY SER LYS GLY GLY ...  
GAAGTGTGTTTAAAGGCCAGCAAGGCGGT...  
430 440 450...

... VAL GLN VAL THR SER THR SER GLU ASN GLY  
... GTGCAGGTACTTCCACCTCTGAACCGGC  
460 470 480

LYS HIS ALA ILE THR PHE ALA LEU ALA LYS ...  
AACACGCCATTACCTTTGCTTTAGCGAA...  
490 500 510...

... ASP LEU ASP MET ARG THR ALA THR VAL SER  
... GACCTTGATATGAGAACTGCCGACTGTGAGT  
520 530 540

ASP THR LEU THR ILE GLY SER THR THR ...  
GATACCTTAACGATTGGCGGTTAGTACT...  
550 560 570...

... THR GLY SER ALA THR THR PRO LYS VAL ASN  
... ACAGGTAGTGCAACAACAACCAAGTGAAAT  
580 590 600

VAL THR SER THR ALA SER GLY LEU ASN PHE ...  
GTGACTAGCAGCGCAAGCGGCTTGAACTTT...  
610 620 630...

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FIG. 22D

FIG. 22D

... ALA LYS GLY ALA THR GLY ALA ASN GLY ASP  
... GCGAAAGGCGCTACAGGTGCTAATGGCGAT  
... 640 650 660

THR THR VAL HIS LEU THR ASN ILE ALA SER ...  
ACTACGGTTCACTTGACTAATAATTGCTTCA...  
670 680 690...  
... THR LEU GIN ASP THR LEU LEU ASN THR GLY  
... ACTTGCAAGATACTCTATTGAAATACTGGG  
... 700 710 720

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VAL VAL SER LYS LEU ASP GLY ASN GLY ILE ...  
GTTGTGAGTAAATTAGATGGTAATGGTATT...  
730 740 750...  
... THR ALA ASP GLU LYS LYS ARG ALA ALA SER  
... ACTGCTGACGAGAAACGCGCGGCAAGC  
... 760 770 780

VAL GLN ASP VAL LEU ASN SER GLY TRP ASN ...  
GTTCAAGATGTTTAAATAAGTGGTTGGAAT...  
790 800 810...  
... ILE LYS GLY VAL LYS THR GLY ALA THR THR  
... ATCAAGGGTGTAAACACAGGTGCGGACCT  
... 820 830 840

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FIG. 22E

FIG. 22E

SER	ASP	ASN	VAL	ASP	PHE	VAL	ARG	THR	TYR	...										
TCT	GAT	AAC	GTT	GAT	TCT	TGTC	CGT	ACT	TAC	...	850									
...	...	...	...	...	...	...	...	...	...	...	860									
...	...	...	...	...	...	...	...	...	...	...	870									
...	...	...	...	...	...	...	...	...	...	...	880									
...	...	...	...	...	...	...	...	...	...	...	890									
...	...	...	...	...	...	...	...	...	...	...	900									
GLU	THR	THR	LEU	VAL	THR	VAL	ASP	SER	GLU	...										
GAA	ACT	AC	ACT	GGT	TAC	AGT	GGT	AGT	GAA	...	910									
...	...	...	...	...	...	...	...	...	...	...	920									
...	...	...	...	...	...	...	...	...	...	...	930									
...	...	...	...	...	...	...	...	...	...	...	940									
...	...	...	...	...	...	...	...	...	...	...	950									
...	...	...	...	...	...	...	...	...	...	...	960									
GLY	ALA	LYS	THR	SER	VAL	ILE	LYS	GLU	LYS	...										
GGT	GGA	AAG	ACC	TCT	GTT	TAT	CAA	GAA	AAA	...	970									
...	...	...	...	...	...	...	...	...	...	...	980									
...	...	...	...	...	...	...	...	...	...	...	990									
...	...	...	...	...	...	...	...	...	...	...	1000									
...	...	...	...	...	...	...	...	...	...	...	1010									
...	...	...	...	...	...	...	...	...	...	...	1020									
LYS	ASP	THR	ASN	GLN	VAL	ALA	SER	ASN	ASN	...										
AAG	ACA	CA	AA	TCA	AGT	CGC	AAG	TAA	TAA	...	1030									
...	...	...	...	...	...	...	...	...	...	...	1040									
...	...	...	...	...	...	...	...	...	...	...	1050									

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FIG.22F

SEQUENCE

... ALA ALA ASP THR ASP GLU GLY LYS GLY  
... GCAGCTGATGATACGGATGAGGGCAAGGC  
... 1060 1070 1080

LEU VAL THR ALA GLU THR VAL ILE ASN ALA ...  
TTAGTCACTGCAGAGACTGTATTCAATGCA...  
1090 1100 1110...  
... VAL ASN LYS ALA GLY TRP ARG ILE LYS THR  
... GTAAACAAGGCTGGTTGGAGAAATTAAACA  
... 1120 1130 1140

THR GLY ALA ASN ASN GLN GLY GLN PHE ...  
ACGGGTGCTAATAATCAAGCTGGTCAGTTT...  
1150 1160 1170...  
... GLU THR VAL THR SER GLY THR ASN VAL THR  
... GAACTGTCAATCAGGCACAAATGTACC  
... 1180 1190 1200

PHE ALA ASP GLY ASN GLY THR ALA VAL ...  
TTGCTGATGGCAATGGTACAACTGCAGTC...  
1210 1220 1230...  
... VAL THR GLY ASP ALA THR ASN GLY ILE THR  
... GTAAGTGGCGATGCTACCAATGGTATTACT  
... 1240 1250 1260

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FIG. 22G

FIG. 22G

VAL LYS TYR GLU ALA LYS VAL GLY ASP GLY ...  
GTTAAATACGAAGCGAAGTTGGCGACGGC...  
1270 1280 1290...

... LEU LYS ILE GLY ASN ASP GLN LYS ILE THR  
... TTGAAGATTGGTAACGACCAAAATCACT  
1300 1310 1320

ALA ASP THR THR ALA LEU THR VAL THR GLY ...  
GCAGATACGACCGCACTTACTGTGACGGC...  
1330 1340 1350...

... GLY LYS VAL THR ALA PRO ASP ALA THR ASN  
... GGTAAAGTTACTGCCCTGATGCAACCAAT  
1360 1370 1380

GLY LYS LYS LEU VAL ASN ALA SER GLY LEU ...  
GGTAAGAACTTGTTAATGCAAGTGGTTTA...  
1390 1400 1410...

... ALA ASP ALA LEU ASN LYS LEU SER TRP THR  
... GCTGATGCCGTTAAACAATAATTAGTTGGACT  
1420 1430 1440

ALA LYS ALA GLU ALA ASP THR ALA ASN GLY ...  
GCAAAAGCTGAAGCAGATACCTGCTAATGGC...  
1450 1460 1470...



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TTTTT"22222222

FIG.22H

... GLY GLU LEU ASP GLY THR ALA ASP GLU LYS  
... GCGAGCTTGATGGAACTGCAGATGAA A A  
... 1480 1490 1500

GLU VAL LYS ALA GLY GLU THR VAL THR PHE ...  
GAAGTTAAGCAGGCGAAACGGTAACCTTT...  
1510 1520 1530...  
... LYS ALA GLY LYS ASN LEU LYS VAL LYS GLN  
... AAGCGGCGAAGAACTTAAAGTGAA A A A  
... 1540 1550 1560

ASP GLY ALA ASN PHE THR TYR SER LEU GLN ...  
GATGGTGCGAACTTTTACTTATTCACCTGCA A...  
1570 1580 1590...  
... ASP ALA LEU THR GLY LEU THR SER ILE THR  
... GATGCTTTAACAGGCTTAACGAGCATTTACT  
... 1600 1610 1620

LEU GLY THR GLY ASN ASN GLY ALA LYS THR ...  
TTAGGTACAGGAAATAATGGTGCGAA A A A C T...  
1630 1640 1650...  
... GLU ILE ASN LYS ASP GLY LEU THR ILE THR  
... GAATCAACAAGACGGCTTAACCATCACA  
... 1660 1670 1680

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FIG. 221

FIG. 221

PRO ALA ASN GLY ALA GLY ALA ASN ASN ALA ...  
CCAGCAAAATGGGTGCGGGTGCAATAATGCA...  
1690 1700 1710...  
... ASN THR ILE SER VAL THR LYS ASP GLY ILE  
... AACACCATCAGCGTAAACCAAGACGGCATT  
1720 1730 1740

SER ALA GLY GLY GIN SER VAL LYS ASN VAL ...  
AGTGCGGCGGTCAGTCGGTTAAACGGTT...  
1750 1760 1770...  
... VAL SER GLY LEU LYS LYS PHE GLY ASP ALA  
... GTGAGCGGACTGAAGAAATTGGTGATGCCG  
1780 1790 1800

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ASN PHE ASP PRO LEU THR SER SER ALA ASP ...  
AATTCGATCCGCTGACTAGCTCCGCCGAC...  
1810 1820 1830...  
... ASN LEU THR LYS GIN TYR ASP ALA TYR  
... AACTTAACGAACAATAATGACGATGCCCTAT  
1840 1850 1860

LYS GLY LEU THR ASN LEU ASP GLU LYS GLY ...  
AAGGCTTGACCAATTGGATGAATAAGGT...  
1870 1880 1890...

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FIG.22J

TABLE 22-29795660

... ALA ASP LYS GLN THR LEU THR VAL ALA ASP  
... GCGGACAAAGCAAACTCTGACTGTGCGGAC  
... 1900 1910 1920

ASN THR ALA ALA THR VAL GLY ASP LEU ARG ...  
AATACTGCCCGCAACCGTGCGGCAATTGCGC...  
1930 1940 1950...

... GLY LEU GLY TRP VAL ILE SER ALA ASP LYS  
... GGC TTGGGCTGGGTCA TTCTGCGGACAA  
... 1960 1970 1980

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THR THR GLY GLU LEU ASP LYS GLU TYR ASN ...  
ACCACAGGCGAATCGATAGGAATACAC...  
1990 2000 2010...

... ALA GLN VAL ARG ASN ALA ASN GLU VAL LYS  
... GCGCAAGTGCGTAACGCCAATGAAGTGAAA  
... 2020 2030 2040

PHE LYS SER GLY ASN GLY ILE ASN VAL SER ...  
TTCAAAGCGGCAACGGTATCAATGTTTCC...  
2050 2060 2070...

... GLY LYS THR VAL ASN GLY ARG ARG GLU ILE  
... GTAAACTGTCAACGGTAGGCGTGAAATT  
... 2080 2090 2100

[illegible]

FIG. 22K

THR PHE GLU LEU ALA LYS GLY GLU VAL ...  
ACTTTTGAATTGGCTAAAGGCGGAAGTGGTT...  
2110 2120 2130...  
... LYS SER ASN GLU PHE THR VAL LYS GLU THR  
... AATCGAATGAATTACTGTCAAAGAAACC  
... 2140 2150 2160

ASN GLY LYS GLU THR SER LEU VAL LYS VAL ...  
AATGGCAAGGAACAAGAGCCTGGTTAAAGTT...  
2170 2180 2190...  
... GLY ASP LYS TYR TYR SER LYS GLU ASP ILE  
... GCGATAAATAATTACAGCAAAGAGGATATTT  
... 2200 2210 2220

ASP PRO ALA THR GLY LYS PRO LYS VAL THR ...  
GACCCAGCAACCGGTAAACCGAAAGTTACA...  
2230 2240 2250...  
... ASN GLY ASN ALA VAL ALA LYS TYR GLN  
... AATGGCAATGCAGTTCCTGCCGAAATATCAA  
... 2260 2270 2280

***SUBSTITUTE SHEET (RULE 26)***

[illegible]

FIG. 22L

[illegible]

ASN LYS GLY TYR GLY THR VAL THR GLY ASN ...  
A A C A A G G T T A T G G C T A T G T A C A G G T A A C ...  
2350 2360 2370...

2360                    2370...  
 ... GIN VAL ALA ASP ALA ILE ALA LYS SER GLY  
 ... C A A G T G G C A G A T G C G A T T G C G A A A T C A G G C  
                          2380                    2390                    2400

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PHE GLU LEU GLY LEU ALA ASP ALA GLU LYS ...  
 TTTGAGCCTTGGTTTGGCTGATGCAGAA...  
 2410 2420 2430...

[illegible]

ALA LEU SER SER ASP LYS LEU GLU THR VAL ...  
GCCCTTGCTCTCTGATAAATTGGAAACCGTA...  
2470 2480 2490...

2480  
... ASN ALA ASN ASP LYS VAL ARG PHE ALA ASN  
... A ATGCCCAACGACAAAGTCCGTTTTGCTAAT  
... 2500 2510 2520

FIG. 22M

FIG. 22M

GLY LEU ASN THR LYS VAL SER ALA THR ...  
GGTTTAAATACCAAGTGAGCGGCAACG...  
2530 2550...  
... VAL GLU SER ILE ASP ALA ASN GLY ASP LYS  
... GTGGAAAGCATCGATGCAAAACGGCGATAAA  
2560 2570 2580

VAL THR THR THR PHE VAL LYS THR ASP VAL ...  
GTGACTACAAACCTTTTGTGAAACCGATGTG...  
2590 2610...  
... GLU LEU PRO LEU THR GIN ILE TYR ASN THR  
... GAATTGCCCTTTAACGCAAAATCTACAATACC  
2620 2630 2640

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ASP ALA ASN GLY LYS LYS ILE VAL LYS ASN ...  
GATGCAACCGGTAAGAAATCGTTAAAAAT...  
2650 2660 2670...  
... GLY ASP LYS TRP TYR TYR THR LYS ASP ASP  
... GGCGATAAATGGTATTACACGAAAGATGAC  
2680 2690 2700

GLY SER THR ASP MET THR LYS GLU VAL THR ...  
GGCTCAACTGATATGACTAAAGAGTTACC...  
2710 2720 2730...

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FIG.22N

446727 299555

... LEU GLY ASN VAL ASP SER ASP GLY LYS LYS  
... CTTGGCAATGTGGATTTCAGACGGCAAGAAA 2760  
... 2740 2750

VAL VAL LYS GLU ASP ASN LYS TRP TYR HIS ...  
GTTGTGAAGAGACAAAGTGGTATCAC... 2770  
... 2790...

... VAL LYS SER ASP GLY SER THR ASP LYS THR  
... GTTAAATCTGATGGTTCTACGGATAAACA 2820  
... 2800 2810

GLN VAL VAL GLU GLU ALA LYS VAL SER THR ...  
CAGGTGGTCCGAAGAGCTAAAGTTTCTACCC... 2830  
... 2840 2850...

... ASP GLU LYS HIS VAL VAL SER LEU ASP PRO  
... GATGAAACACACGTTGTTCAGCCTTGATCCA 2880  
... 2860 2870

ASN ASP GLN SER LYS GLY LYS VAL VAL ...  
AATGATCAATCAAAAGGTAAAGGCGTGGTC... 2890  
... 2910...

... ILE ASN MET ALA ASN GLY GLU ILE SER  
... ATTAACAATATGGCTAATGGCGAAATTCTT 2940  
... 2920 2930

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FIG.220

FIG.220 "2974666"

ALA	THR	SER	THR	ASP	ALA	ILE	ASN	GLY	SER	...	
GCC	ACT	TTC	ACC	GAT	GCG	ATT	AAC	GGA	AGT	...	
										2950	
...	GLN	LEU	TYR	ALA	VAL	ALA	LYS	GLY	VAL	THR	
...	CAG	TTG	TAT	GCC	GTT	GCA	AAA	AGG	GTA	ACA	
...											3000
											2980
ASN	LEU	ALA	GLY	GLN	VAL	ASN	ASN	LEU	GLU	...	
AAC	CTT	GCT	TGG	ACA	AGT	GAA	TAA	TCT	TGA	G...	
										3010	
...	GLY	LYS	VAL	ASN	LYS	VAL	GLY	LYS	ARG	ALA	
...	GGC	AAA	AGT	GAA	TAA	AGT	GCG	CAA	ACG	TGC	
...											3060
											3040
ASP	ALA	GLY	THR	ALA	SER	ALA	LEU	ALA	ALA	...	
GAT	GAG	GTA	CTG	CAAG	TGCA	TTAG	CGGC	T...			
										3070	
...	SER	GLN	LEU	PRO	GLN	ALA	THR	MET	PRO	GLY	
...	TCA	CAG	TAC	CA	CAAG	CCACT	ATG	CCAGG	T		
...											3120
											3110
LYS	SER	MET	VAL	SER	ILE	ALA	GLY	SER	SER	...	
AA	TCA	ATG	GTT	TCT	TAT	TGCG	GGA	AGT	AGT	...	
										3130	
											3150...



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FIG.22P

TTTATT TTTTGGG

... TYR GIN GLY GIN ASN GLY LEU ALA ILE GLY  
... TATCAAGGTCAAAATGGTTTAGCTATCGGG  
... 3160 3170 3180

VAL SER ARG ILE SER ASP ASN GLY LYS VAL ...  
GTATCAAGAAATTTCCGATAATGGCAAGTG...  
... 3190 3200 3210...  
... ILE ILE ARG LEU SER GLY THR ASN SER  
... ATTATTCGCTTGTCAAGGCACACCAATAGT  
... 3220 3230 3240

GIN GLY LYS THR GLY VAL ALA ALA GLY VAL ...  
CAAGGTAAACAAGCGCTTGCAGCAGGTGT...  
... 3250 3260 3270...  
... GLY TYR GIN TRP \*\*\*  
... GGTTACCAGTGGTAATAGAAATCCGGATCC  
... 3280 3290 3300

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# FIG.23A

NTHi strain K22 Hia

MET ASN LYS ILE PHE ASN...  
GCGAATTCATATGAACAAATTTTAA...  
10 20 ...  
... VAL ILE TRP ASN VAL THR GLN THR TRP VAL  
...CGTTATTGGAAATGTTGTGACTCAAACTTGGGT 50 60  
... 30 40

VAL VAL SER GLU LEU THR ARG ALA HIS...  
TGTCGTATCTGAACACTCACTCGGCCCA...  
70 80 ...  
... THR LYS CYS ALA SER ALA THR VAL ALA VAL ALA  
...CACCAAATGCGCCCTCCGCCACCGTGGCGGTGTC 110 120  
... 90 100

VAL LEU ALA THR ALA LEU SER ALA THR...  
CGTATTGGCAACTGCGTTGTCTGCAAC...  
130 140 ...  
... ALA GLU ALA ASN ASN THR SER VAL THR ASN  
...GGCTGAGCGGAACAACAATACTTCTGTACGAA 170 180  
... 150 160

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FIG.23B

GLY LEU ASN ALA TYR GLY ASP THR ASN...  
TGGGTTGAATGCTTATGGCGATACTAA...  
190 ...  
... PHE ASN THR THR ASN ASN SER ILE ALA ASP LEU  
...TTTAAATACAAACCAATAATTTCGATAGCAGATT  
... 210 220 230 240

GLU LYS HIS VAL GIN ASP ALA TYR LYS...  
GGAAACACACGTTCAAGATGCTTATAA...  
250 ...  
... GLY LEU LEU ASN LEU ASN GLU LYS ASP THR ASN  
...AGGCTTATTAAATCTGAATGAATAAGATACAAA  
... 270 280 290 300

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LYS SER SER PHE LEU VAL ALA ASP ASN...  
TAAGTCAAGTTTCTTGGTTGCCGACAA...  
310 ...  
... THR ALA ALA THR VAL GLY ASN LEU ARG LYS LEU  
...TACCGCCGCAACCGTAGGCAATTTCGTAATT  
... 330 340 350 360

GLY TRP VAL LEU SER SER LYS ASN GLY...  
GGGCTGGGTATTGTCTAGCAAAACGG...  
370 380 ...

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FIG.23C

THE PATENT OFFICE

... THR ARG ASN GLU LYS SER TYR GIN VAL LYS GIN  
...CACAAGGAACGAGAAAGCTATCAAGTAAACA  
... 390 400 410 420

ALA ASP GLU VAL LEU PHE THR GLY SER...  
AGCTGATGAAGTTCTCTTTTACTGGATC...  
430 440

... GLY ALA ALA THR VAL SER SER SER LYS ASP  
...TGGTGCTGCACCGGTTAGTTCCAGCTCTAAAGA  
... 450 460 470 480

GLY LYS HIS THR ILE THR ILE SER VAL...  
CGGTAAACATACCATTTACCATTTCTGT...  
490 500

... THR LYS GLY SER PHE ALA GLU VAL LYS THR ASP  
...TACCAGGAGTAGTTTGTGCTGAGGTAAACTGA  
... 510 520 530 540

ALA THR THR GLY GLY VAL ASN ALA...  
TGCAACTACTGGAGGTCAAGTAAACGC...  
550 560

... ASP ARG GLY LYS VAL LYS ALA GLU ASP GLU ASN  
...CGACCGTGGTAAAGTGAAAGCTGAGGACGAGAA  
... 570 580 590 600

FIG. 23D

FIG.23D

GLY ALA ASP VAL ASP LYS LYS VAL ALA...  
TGGAGCTGATGTTGATAAGAAAGTTGC ...  
610 620

... THR VAL LYS ASP VAL ALA LYS ALA ILE ASN ASP  
...A ACTGTAAAGATGTTGCTAAGGCGATTAAACGA  
... 630 640 650 660

ALA ALA THR PHE VAL LYS VAL GLU SER...  
TGCCGCAACTTTCGTGAAAGTGGAAG ...  
670 680

... THR ASP ASP ILE GLU ASN GLY ALA ALA GLY  
...CACAGATGATGACATTGAAATAATGGTGCTGCAGG  
... 690 700 710 720 101/204

LYS ASN GLU THR THR ASP GLN ALA LEU...  
CAAAATGAACCTACAGACCAAGCTCT ...  
730 740

... LYS ALA GLY ASP THR LEU THR LEU LYS ALA GLY  
...CAAGCAGCGCACCTTAACCTTAAAGCGGG  
... 750 760 770 780

LYS ASN LEU LYS ALA LYS LEU ASP GLN...  
TAAAAACTTAAAGCTAAGTTAGACCA ...  
790 800

FIG. 23E

FIG.23E

... ASN GLY LYS SER VAL THR PHE ALA LEU ALA LYS  
...AATGGTAAATCAGTAACCTTTGCTTTAGCGAA 840  
... 810 820 830

ASP LEU ASP VAL THR SER ALA LYS VAL...  
AGACCTTGATGTGACCTCTGCGAAAGT...

... 850 860  
... SER ASP LYS LEU SER ILE GLY LYS ASP THR ASN  
...GAGTGATAAGTTGTCTATTGGTAAAGATACGAA 900  
... 870 880 890

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LYS VAL ASP ILE THR SER ASP ALA ASN...  
TAAAGTTGATATTACCAAGTGCAAA...

... 910 920  
... GLY LEU LYS LEU ALA LYS THR GLY ASN GLY ASN  
...TGGCTTGAAATTGGCGAAACACAGGTACGGAAA 960  
... 930 940 950

GLY GLN ASN GLY ASN VAL HIS LEU ASN...  
TGGTCAAAACGGTAATGTCCTCACTTAA...

... 970 980  
... GLY ILE ALA SER THR LEU THR ASP THR ILE THR  
...TGGTATTGCTTCGACTTTGACCGATACCATAC 1020  
... 990 1000 1010

FIG. 23F

FIG.23F

GLY MET THR THR GIN ALA SER ASN GLY...  
AGGTATGACACACACAGCAAGCAATGG...  
1030  
... VAL ALA VAL GIN ASN HIS ASN ARG ALA ALA SER  
1040  
...CGTGGCTGTGCAGAAATCATATCCTGCTGCGAG  
1050  
... 1060 1070 1080

VAL ALA ASP VAL LEU ASN ALA GLY TRP...  
TGTGGCTGATGTATTAAATGCAGGCTG...  
1090  
... ASN ILE GIN GLY ASN GLY ALA SER VAL ASP PHE  
1100  
...GAAATATTCAAGGCAACGGAGCGGCTTGATTT  
1110  
... 1120 1130 1140

VAL ASN ALA TYR ASP THR VAL ASP PHE...  
TGTCAATGCTTACGACACAGTAGATT...  
1150  
... VAL ASN GLY THR ASN THR ASN VAL ASN VAL THR  
1160  
...TGTCAATGGTACAAACACCAATGTGAACGTAC  
1170  
... 1180 1190 1200

THR ASP THR ALA HIS LYS LYS THR THR...  
GACTGATACGGCTCACAAAGAGACAC...  
1210  
... 1220

FIG. 23G

FIG.23G

... VAL ARG VAL ASP VAL THR GLY LEU PRO VAL GLN  
...CGTCCGTGTGGATGTAAACAGGCTTGCCGGTTCA 1260  
... 1230 1240 1250

TYR VAL THR GLU ASP GLY LYS THR VAL...  
ATATGTTACGGAGACGGCAAAACCGT... 1270  
... 1280

... VAL LYS VAL ASP ASN LYS TYR TYR GLU ALA LYS 104/204  
...TGTGAAGTGGACAATAAGTATTACGAAGCTAA 1320  
... 1290 1300 1310

GLN ASP GLY SER ALA ASP MET ASP LYS...  
GCAAGACGGTTCGGCGGATATGGATAA... 1330  
... 1340

... LYS VAL GLU ASN GLY GLU LEU ALA LYS THR LYS  
...AAAGTCGAAATAAGCGAGCTGGCGAATAACCAA 1380  
... 1350 1360 1370

VAL LYS LEU VAL SER ALA SER GLY GLN...  
AGTGAAATTGGTGTCTGGCAAGCGGTCA... 1390  
... 1400

... ASN PRO VAL LYS ILE SER ASN VAL ALA GLU GLY  
...AATCCGGTGAAAATCAGCAATGTTCGGGAAGG 1440  
... 1410 1420 1430



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FIG.23H

THR GLU GLU THR ALA SER ASN ASP ALA VAL SER PHE...  
CACGGAAGAAACGATGCGGTCAGCTT...  
1450  
... LYS GLN LEU LYS ALA LEU GLN GLY LYS GLN VAL  
...TAAGCAATTGAAGCCCTTGCAAGAGAAACAGGT  
1460  
... 1470 1480 1490 1500

THR LEU THR THR ALA SER ASN ALA TYR ALA...  
TACTTTAACTGCGAGCAATGCTTATGC...  
1510  
... ASN GLY GLY ASN ASP ALA ASP GLY GLY LYS ALA  
...CAATGGTGGTAACGATGCCGACGGCGCAAGGC  
1520  
... 1530 1540 1550 1560

THR GLN THR THR LEU ASN GLY LEU ASN...  
AACTCAAACTTTAAACAATGTTTGAA...  
1570  
... PHE LYS PHE LYS SER THR ASP GLY GLU LEU LEU  
...TTTAAATTAAATCCACAGACGGCGAGTTGTT  
1580  
... 1590 1600 1610 1620

ASN ILE LYS VAL GLU ASN ASP THR VAL...  
GAACATCAAGTAGAAATGACACAGT...  
1630  
... 1640

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FIG. 23I

FIG.23I

... THR PHE THR PRO LYS LYS GLY SER VAL GLN VAL  
...TACCTTTACGCCGAAATAAGGTTTCGGTACAGGT 1670  
... 1650 1660 1670 1680

GLY GLU ASP GLY LYS ALA THR ILE GLN...  
TGGCGAAGACGGTAAGGCTACGATTCA... 1690  
... 1700

... ASN GLY THR LYS THR THR ASP GLY LEU VAL GLU  
...AATGGTACGAAACAACCCGACGGTTTGGTTGA 1730  
... 1710 1720 1740

ALA SER GLU LEU VAL GLU SER LEU ASN...  
AGCTTCCGAATTGGTTGAAAGCCTGAA... 1750  
... 1760

... LYS LEU GLY TRP LYS VAL GLY VAL ASP LYS ASP  
...CAACTGGGCTGGAAAGTGGGCGTTGATAAAGA 1790  
... 1770 1780 1800

GLY SER GLY GLU LEU ASP GLY ALA SER...  
CGGCAGCGCGAGCTTGATGGTGCAATC... 1810  
... 1820

... ASN GLU THR LEU VAL LYS SER GLY ASP LYS VAL  
...CAATGAACCTTTAGTGAGTCCGGCGGATAAAGT 1850  
... 1830 1840 1860

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[illegible]

**FIG.23J**

[illegible]

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FIG.23K

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... LYS ILE LYS VAL ALA SER ASP GLY ILE SER ALA  
...CAAGATTAAAGTGGCTTCAGACGGCATCAGTGC 2100  
... 2070 2080 2090

GLY ASN LYS ALA VAL LYS ASN VAL VAL...  
GGGTAAATAAGCGGTTTAAACGTTGT... 2110  
... 2120 ...  
... SER GLY LEU LYS LYS PHE GLY ASP ALA ASN PHE  
...GAGCGGACTGAAGAAATTTGGTGATGCCAATT 2160  
... 2130 2140 2150

ASN PRO LEU THR SER SER ALA ASP ASN...  
CAATCCACTGACCCAGTTCCGCCGACAA... 2170  
... 2180 ...  
... LEU THR LYS GLN TYR ASP ASP ALA TYR LYS GLY  
...CTTAACGAACAATATGACGATGCCCTATAAAG 2220  
... 2190 2200 2210

LEU THR ASN LEU ASP GLU LYS GLY ALA...  
CTTGACCAATTGGATGAATAAGGTGC... 2230  
... 2240 ...  
... ASP LYS GLN THR LEU THR VAL ALA ASP ASN THR  
...GGACAAGCAACTCTGACTGTGCGCAATAC 2280  
... 2250 2260 2270

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FIG. 23L

FIG. 23L

ALA ALA THR VAL GLY ASP LEU ARG GLY...  
T G C C G C A A C C G T G G G C G A T T T G C G C G ...  
2290 2300 ...  
... LEU GLY TRP VAL ILE SER ALA ASP LYS THR THR  
... C T T G G G C T G G G T C A T T T C T G C G G A C A A A C C A C  
... 2310 2320 2330 2340

GLY GLU LEU ASN LYS GLU TYR ASN ALA...  
A G G C G A A C T C A A T A A G G A A T A C A C G C ...  
2350 2360 ...  
... GLN VAL ARG ASN ALA ASN GLU VAL LYS PHE LYS  
... G C A A G T G C G T A A C G C C A A T G A A G T G A A A T T C A A  
... 2370 2380 2390 2400

SER GLY ASN GLY ILE HIS VAL SER GLY...  
G A G C G C A A C G G T A T C C A T G T T T C C G G ...  
2410 2420 ...  
... LYS THR VAL ASN GLY ARG ARG GLU ILE THR PHE  
... T A A A C G G T C A A C G G T A G G C G C G A A A T T A C T T  
... 2430 2440 2450 2460

GLU LEU ALA LYS ASP GLU ASN ALA ILE...  
T G A A T T G G C T A A A G A C G A A A A T G C C A T ...  
2470 2480 ...

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TDGTTT 00000000

FIG.23M

... ALA PHE GLY TYR GLY SER LYS ALA LEU ARG ASP  
...TGCTTTCGGTTATGGCTCAAAAGCCTTGCGCGA 2520  
... 2490 2500 2510

ASN THR VAL ALA ILE GLY THR GLY ASN...  
TAACACGGTGGCAATTGGTACGGGCAA... 2530  
... 2540

... VAL VAL ASN ALA GLU LYS SER GLY ALA PHE GLY  
...CGTTGTGAATGCGGAAATACTGGTGCAATTCGG 2580  
... 2550 2560 2570

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ASP PRO ASN TYR ILE GLU ASP LYS ALA...  
CGATCCGAACATACATCGAAGATAAAGC... 2590  
... 2600

... GLY GLY SER TYR ALA PHE GLY ASN ASP ASN ARG  
...CGGTGGCAGCTACGCTTTCGGTAACGATAACCG 2640  
... 2610 2620 2630

ILE THR SER LYS ASN THR PHE VAL LEU...  
TATTACTTCTAAACACACTTTTGTT... 2650  
... 2660

... GLY ASN GLY VAL ASN ALA LYS TYR LYS ALA ASN  
...GGGTAATGGAGTTAATGCGAAATATAAGCCAA 2700  
... 2670 2680 2690

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TABLE 21-29E9E669

FIG.23N

GLY ASP VAL ASP THR GLU THR VAL THR...  
TGGAGATGTTGATACGGAAACCGTAC...  
2710 ... VAL LYS ASP LYS ASP GLY LYS GLU THR THR VAL  
...CGTTAAGGACAAAGACGGTAAAGAGACTACCGT 2750  
... 2730 2740 2760

THR VAL PRO LYS LYS ALA LEU GLY ALA THR...  
TACTGTTCCCTAAAGCGTTAGGGGTAC...  
2770 ... VAL GLU ASN SER VAL TYR LEU GLY ASN LYS SER  
...GTTTGAAACCTCCGTTTATTGGGGTAATAAATC 2820  
... 2790 2800 2810 2820

THR ALA THR LYS LYS ASP LYS GLY LYS ASN...  
GACTGCGACAAAGATAGGGGTAAAAA...  
2830 ... LEU LYS SER ASP GLY THR ALA GLY ASN THR THR  
...CCTGAAATCTGATGGTACGGCGGGGTAACTACTAC 2880  
... 2850 2860 2870 2880

THR ALA GLY THR THR GLY THR VAL ASN...  
AACTGCTGGCACAAACGGGTACGGTAA...  
2890 ... 2900

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FIG.230

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... GLY PHE ALA GLY ALA THR ALA HIS GLY ALA VAL  
...CGGCTTTGCCGGTGCACCGCGCACGGTGCGGT 2940  
... 2910 2920 2930

SER VAL GLY ALA SER GLY GLU ARG...  
TTCTGTCGGCGCAAGCGCGAAGAAAG... 2950  
... 2960  
... ARG ILE GIN ASN VAL ALA ALA GLY GLU ILE SER  
...ACGTATCCAAACGTCGCGGCAGCGAATTTC 3000  
... 2970 2980 2990

ALA THR SER THR ASP ALA ILE ASN GLY...  
CGCCACTTCCACCGATGCGGATTACGG... 3010  
... 3020  
... SER GIN LEU TYR ALA VAL ALA LYS GLY VAL THR  
...CAGCCAGTTGTATGCTGTGGCAAAAGGGGTAC 3060  
... 3030 3040 3050

ASN LEU ALA GLY GIN VAL ASN LYS VAL...  
AATCTTGCTGGACCAAGTGAAATAAGT... 3070  
... 3080  
... GLY LYS ARG ALA ASP ALA GLY THR ALA SER ALA  
...GGGCAACCGTGCAGATGCAGGTACAGCAAGTGC 3120  
... 3090 3100 3110



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FIG.23P

LEU ALA ALA SER GIN LEU PRO GIN ALA...  
ATTAGCAGCTTACACAGTTACCAAGC...  
3130  
... SER MET PRO GLY LYS SER MET VAL SER ILE ALA  
...CTCTATGCCAGGTAAATCAATGGTTTCTATTGC  
3150 3160 3170 3180

GLY SER SER TYR GIN GLY GIN ASN GLY...  
GGGAAGTAGTTATCAAGGTCAAAATGG...  
3190  
... LEU ALA ILE GLY VAL SER ARG ILE SER ASP ASN  
...TTTAGCTATCGGGGTATCAGCAATTTCGGATAA  
3210 3220 3230 3240

GLY LYS VAL ILE ILE ARG LEU SER GLY...  
TGGCAAGTGATTTATTCGCTTGTCAGG...  
3250  
... THR THR ASN SER GIN GLY LYS THR GLY VAL ALA  
...CAACAACCAATAGCCAAGGTAAACAGGCGTTGC  
3270 3280 3290 3300

ALA GLY VAL GLY TYR GIN TRP \*\*\*  
AGCAGGTGTTGGTTACCAAGTGGTAATA...  
3310 3320  
...GAATTGATCCGC  
... 3330

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*H. influenzae* type c strain API hia sequence

***SUBSTITUTE SHEET (RULE 26)***

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FIG.24B

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... HIS SER ASP LYS GLU GLY THR GLY GLU LYS  
... CATTCCGATAAAGAGGCGACGGGAGAAAAA 240  
... 220 230

GLU VAL THR GLU ASN SER ASN TRP GLY ILE ...  
GAAGTTACAGAAAATTCAAAATTGGGGAATA... 250  
... 260 270...  
... TYR PHE HIS ASN LYS GLY VAL LEU LYS ALA  
... TATTCCACAATAAAGGAGTACTAAAGCC 300  
... 280 290

GLY ALA ILE THR LEU LYS ALA GLY ASP ASN ...  
GGAGCAATCACCTCAAAAGCCGGCGACAC... 310  
... 320 330...  
... LEU LYS ILE LYS GLN SER THR ASN ALA SER  
... CTGAAAATCAAAACAAAGCACCAATGCCAGT 360  
... 340 350

SER PHE THR TYR SER LEU LYS ASP LEU ...  
AGCTTCACTACTCGCTGAAAAAAGACCTC... 370  
... 380 390...  
... THR ASP LEU THR SER VAL ALA THR GLU LYS  
... ACAGATCTGACCAAGTGTTGCAACTGAAAAA 420  
... 400 410

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FIG. 24C

FIG. 24C

LEU SER PHE GLY ALA ASN GLY ASP LYS VAL ...  
TTATCGTTTGGCGCAACGGCGATAAAGTT...  
430 440 450...  
... ASP ILE THR SER ASP ALA ASN GLY LEU LYS  
... GATATTACCAGTGATGCAAAATGGCTTGAAA  
460 470 480

LEU ALA LYS THR GLY ASN GLY ASN VAL HIS ...  
TTGGCGAAACACAGGTAACGGAAATGTTTCAT...  
490 500 510...  
... LEU ASN GLY LEU ASP SER THR LEU PRO ASP  
... TTGAATGGTTTGGGATTCACCTTGCCCTGAT  
520 530 540 550

ALA VAL THR ASN THR GLY VAL LEU SER SER ...  
GCGGTAACGAAATACAGGTGTGTAAAGTTCA...  
550 560 570...  
... SER SER PHE THR PRO ASN ASP VAL GLU LYS  
... TCAAGTTTACACCTAATGATGTTGAAAAA  
580 590 600

THR ARG ALA ALA THR VAL LYS ASP VAL LEU ...  
ACAAGAGCTGCAACTGTGTTAAAGATGTTTAA...  
610 620 630...

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FIG.24D

SEQUENCE

... ASN ALA GLY TRP ASN ILE LYS GLY ALA LYS  
... AATGCAGGTTGGAAACATTTAAAGGTGCTAAA 660  
... 640

THR ALA GLY GLY ASN VAL GLU SER VAL ASP ...  
ACTGCTGGAGGTAATGTTGAGAGTGTGAT... 680  
... 670  
... LEU VAL SER ALA TYR ASN ASN VAL GLU PHE  
... TTAGTGTCCTTATAATAATGTTGAAATTT 720  
... 700

ILE THR GLY ASP LYS ASN THR LEU ASP VAL ...  
ATTACAGGCGATAAACAACGCTTGATGT... 740  
... 730  
... VAL LEU THR ALA LYS GLU ASN GLY LYS THR  
... GTATTACAGCTAAAGAAACGGTAACA 780  
... 760

THR GLU VAL LYS PHE THR PRO LYS THR SER ...  
ACCGAAGTGAAATTCAACCGAAACCTCT... 800  
... 790  
... VAL ILE LYS GLU LYS ASP GLY LYS LEU PHE  
... GTTATCAAGAAAGACGGTAAGTTATTT 840  
... 820

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[illegible]

FIG. 24E

THR	GLY	LYS	GLU	ASN	ASP	THR	ASN	LYS	...
ACT	GAA	AAG	AGA	ATA	CAC	CAA	ATA	AAA...	
								870...	
					860				
				...	VAL	THR	SER	ASN	THR
				...	GTT	ACA	GTA	ACA	CGCG
				...					ACT
				...					GTA
				...					ATAC
				...					ACA
				...					900

[illegible]

TRP ARG VAL LYS THR THR THR ALA ASN GLY ...  
TGGAGAGTTAAACAAC TACTGCTAATGGT...  
970 980 990...  
... GLN ASN GLY ASP PHE ALA THR VAL ALA SER  
... CAAATGGCGACTTCGCACTGTGCGTCA  
1000 1010 1020

GLY THR ASN VAL THR PHE GLU SER GLY ASP ...  
G G C A C A A A T G T A C C T T G A A A G T G C G A T ...  
1030 1040 1050...

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THE "SECRET"

FIG.24F

... GLY THR THR ALA SER VAL THR LYS ASP THR  
... GGTACAACAGCGTCAGTAACTAAGATACT 1080  
... 1060 1070

ASN GLY ASN GLY ILE THR VAL LYS TYR ASP ...  
AACGGCAATGGCATCTACTGTTAAGTACGAC... 1100  
... ALA LYS VAL GLY ASP GLY LEU LYS PHE ASP  
... CGGAAGTTGGCGACGGCTTGAAATTTGAT 1140  
... 1120 1130

SER ASP LYS LYS ILE VAL ALA ASP THR ...  
AGCGATAAATAATCGTTGCAGATACGACC... 1160  
... ALA LEU THR VAL THR GLY LYS VAL ALA  
... GCACTTACTGTGACAGGTGGTAAGGTAGCT 1200  
... 1180 1190

GLU ILE ALA LYS GLU ASP LYS LYS ...  
GAATTGCTAAAGAGATGACAGAAATAA... 1210  
... LEU VAL ASN ALA GLY ASP LEU VAL THR ALA  
... CTTGTTAATGCAAGCGGATTTGGTAACAGCT 1260  
... 1230 1240 1250

FIG. 24G

FIG. 24G

LEU GLY ASN LEU SER TRP LYS ALA LYS ALA ...  
TTAGGTAATCTAAGTTGGAAAGCAAGCT...  
1270 1280 1290...  
... GLU ALA ASP THR ASP THR ASP GLY ALA LEU  
... GAGGCTGATACTGATGATGATGGTGGCTT  
1300 1310 1320

GLU GLY ILE SER LYS ASP GIN GLU VAL LYS ...  
GAGGGGATTTCAAAAGACCAAGAGTCAA...  
1330 1340 1350...  
... ALA GLY GLU THR VAL THR PHE LYS ALA GLY  
... GCAGGCGAAACGGTAACCTTTAAGCGGGC  
1360 1370 1380

LYS ASN LEU LYS VAL LYS GIN ASP GLY ALA ...  
AAGAACTTAAAGTGAAACAGGATGGTGG...  
1390 1400 1410...  
... ASN PHE THR TYR SER LEU GIN ASP ALA LEU  
... AACCTTACTTATTCACCTGCAAGATGCTTTA  
1420 1430 1440

THR GLY LEU THR SER ILE THR LEU GLY ...  
ACGGGTTTAACGAGCATTTACTTTAGGTGGT...  
1450 1460 1470...



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FIG.24H

SEQUENCE

... THR THR ASN GLY GLY ASN ASP ALA LYS THR  
... ACAACTAATGGCGGAAATGATGCGAAACC 1500  
... 1480 1490

VAL ILE ASN LYS ASP GLY LEU THR ILE THR ...  
GTCAACAACAAGACGGTTTAACCATCAG... 1510  
... 1520 1530...

... PRO ALA GLY ASN GLY GLY THR THR GLY THR  
... CCAGCAGGTAATGGCGGTACGACAGGTACA 1560  
... 1540 1550

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ASN THR ILE SER VAL THR LYS ASP GLY ILE ...  
AACACCATCAGCGTAACCAAGATGGCAATT... 1570  
... 1580 1590...

... LYS ALA GLY ASN LYS ALA ILE THR ASN VAL  
... AAGCAGGTAATAAGCTATTACTAATGTT 1620  
... 1600 1610

ALA SER GLY LEU ARG ALA TVR ASP ALA ...  
GCGAGTGGTTTAAGAGCTTATGACGATGCG... 1630  
... 1640 1650...

... ASN PHE ASP VAL LEU ASN ASN SER ALA THR  
... AATTTGATGTTTAAATAACTCTGCACT 1680  
... 1660 1670

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1690 1700 1710 1720 1730 1740

FIG.24I

ASP LEU ASN ARG HIS VAL GLU ASP ALA TYR ...  
GATTTAAATAGACACGTTGAGATGCTTAT...  
1690 1700 1710 1720 1730 1740  
... LYS GLY LEU LEU ASN LEU ASN GLU LYS ASN  
... AAGGTTTATTAAATCTAAATGAAAAAT  
... 1720 1730 1740

ALA ASN LYS GIN PRO LEU VAL THR ASP SER ...  
GCAATAAACACACCGTTGGTGACTGACAGC...  
1750 1760 1770 1780 1790 1800  
... THR ALA ALA THR VAL GLY ASP LEU ARG LYS  
... ACGCGGCGACTGTAGGCGATTACGTAA  
... 1780 1790 1800

LEU GLY TRP VAL VAL SER THR LYS ASN GLY ...  
TTGGGTTGGGTAGTATCAACCAAAACGGT...  
1810 1820 1830 1840 1850 1860  
... THR LYS GLU GLU SER ASN GIN VAL LYS GIN  
... ACGAAAGAGAAAGCAATCAAGTTAAACAA  
... 1840 1850 1860

ALA ASP GLU VAL VAL PHE THR GLY ALA GLY ...  
GCTGATGAAGTCTCTTTACCGGAGCCGGT...  
1870 1880 1890 1900

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[illegible]

FIG. 24J

	ALA	ALA	THR	VAL	THR	SER	LYS	SER	GLU	ASN
.....	GCT	GCT	ACG	GTT	ACT	TCC	AAA	TCT	GAA	AAC
	1900		1910		1920					

[illegible]

ASP	GLY	ASP	THR	ILE	LYS	LEU	LYS	VAL	ASP ...
GAT	GCG	GAT	ACT	ATT	AGC	TCA	AGT	GGA	T...
1990									
2000									
2010...									
...									
ASN	GLN	ASN	THR						
...									
ATA	TCA	AA	CA	CA	CA	CA	CA	CA	CT
2020									

GLY ASN ASN GLY THR ALA VAL THR LYS GLY ...  
 GGTAAATAATGGTACTGCTGCTAAAGGT...  
 2050 2060 2070...  
 ... GLY PHE GLU THR VAL LYS THR GLY ALA THR  
 ... GGCTTTGAAACTGTTAAAACTGGAGCGACT  
 2080 2090 2100

[illegible]

FIG. 24K

```

ASP  ALA  ASP  ARG  GLY  LYS  VAL  THR  VAL  LYS  ...
GAT  GCA  GAT  CGC  GGT  AAG  TAA  CTG  TAA  A...
                                     2110
                                     2120
                                     2130...
...  ASP  ALA  THR  ALA  ASN  ASP  ALA  ASP  LYS  LYS
...  GAT  GCT  ACT  GCT  AAT  GAC  CGC  TGA  TAA  GAA  A
                                     2140
                                     2150
                                     2160

```

[illegible]

GLU ASN LEU THR THR SER ILE ASP GLU ASP ...  
 GAG AATTTAACTACTCTCTATTGATGAGAT...  
 2230 2240 2250...  
 ... ASN PRO THR ASP ASN GLY LYS ASP ASP ALA  
 ... AATCCTACAGATTAACGGCAAGATGACGCA  
 2260 2270 2280

LEU LYS ALA GLY ASP THR LEU THR PHE LYS ...  
C T T A A G C G G G C G A T A C C T T A C C T T A A A ...  
2290 2300 2310...

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TABLE "PHEBESN"

FIG.24L

... ALA GLY LYS ASN LEU LYS VAL LYS ARG ASP  
... GCAGGTAAACCTGAAAGTTAAACGTGAT 2340  
... 2320 2330

GLY LYS ASN ILE THR PHE ASP LEU ALA LYS ...  
GGAATAATATTACTTTTGACTTGGCGAAA... 2350  
... 2360 2370...

... ASN LEU GLU VAL LYS THR ALA LYS VAL SER  
... AACCTTGAGGTGAAACTGCCGAAAGTGAGT 2400  
... 2380 2390

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ASP THR LEU THR ILE GLY ASN THR PRO ...  
GATACCTTAAACGATTGGCGGGAATACACCT... 2410  
... 2420 2430...

... THR GLY GLY THR THR ALA THR PRO LYS VAL  
... ACAGGTGGCACTACTGCGACGCCAAAGTG 2460  
... 2440 2450

ASN ILE THR SER THR ALA ASP GLY LEU ASN ...  
AATACTACTAGCACGGCTGATGGTTTGAAAT... 2470  
... 2480 2490...

... PHE ALA LYS GLU THR ALA ASP ALA SER GLY  
... TTGCAAAAGAAACAGCCGATGCCCTCGGGT 2520  
... 2500 2510

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TABLE 2959565

FIG.24M

SER LYS ASN VAL TYR LEU LYS GLY ILE ALA ...  
TCTAAGAAATGTTTATTGAAAGGTATTGCG...  
2530 2540 2550...  
... THR THR LEU THR GLU PRO SER ALA GLY ALA  
... ACAACTTTAACTGAGCCCAAGCGGAGCGG  
2560 2570 2580

LYS SER SER HIS VAL ASP LEU ASN VAL ASP ...  
AAGTCTTCACACGTTGATTATAATGTGGAT...  
2590 2600 2610...  
... ALA THR LYS LYS SER ASN ALA ALA SER ILE  
... GCGACGAAATAATCCAAATGCAGCAAGTATT  
2620 2630 2640

GLU ASP VAL LEU ARG ALA GLY TRP ASN ILE ...  
GAAGATGTATTGCGCGCAGGTGGAAATATT...  
2650 2660 2670...  
... GLN GLY ASN GLY ASN ASN VAL ASP TYR VAL  
... CAAAGTAATGGTAATAATGTTGATTATGTA  
2680 2690 2700

ALA THR TYR ASP THR VAL ASN PHE THR ASP ...  
GCGACGTATGACACAGTAACCTTTACCGAT...  
2710 2720 2730...

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TABLE 2959660

FIG.24N

... ASP SER THR GLY THR THR THR VAL VAL  
... GACAGCACAGGTACAAACACGGTAACCGTA 2760  
... 2740 2750

THR GLN LYS ALA ASP GLY LYS GLY ALA ASP ...  
ACCCAAAGCAGATGGCAAAAGGTGCTGAC... 2780  
... VAL LYS ILE GLY ALA LYS THR SER VAL ILE 2820  
... GTTAAATCGGTGCCGAAACACTTCTGTATC 2810  
... 2800

LYS ASP HIS ASN GLY LYS LEU PHE THR GLY ...  
AAGACCAACAACGGCAAACTGTTTACAGGC... 2840  
... LYS ASP LEU LYS ASP ALA ASN ASN GLY ALA 2880  
... AAGACCTGAAAGATGCCGAATAATGGTCCA 2870  
... 2860

THR VAL SER GLU ASP ASP GLY LYS ASP THR ...  
ACCGTTAGTGAAGATGATGGCAAGACACCC... 2900  
... GLY THR GLY LEU VAL THR ALA LYS THR VAL 2940  
... GGCAACAGGCTTAGTTACTGCCAAACTGTG 2930  
... 2920

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FIG.240

ILE ASP ALA VAL ASN LYS SER GLY TRP ARG ...  
ATTGATGCAGTAATAATAAGCGGTGGAGG...  
2950 2960 2970...  
... VAL THR GLY GLU GLY ALA THR ALA GLU THR  
... GTAAACCGGTGAGGCGCGACTGCCGAAC 2980 2990 3000

GLY ALA THR ALA VAL ASN ALA GLY ASN ALA ...  
GGTGCAACCGCGGTGAATGCGGGTAACGCT...  
3010 3020 3030...  
... GLU THR VAL THR SER GLY THR SER VAL ASN  
... GAACCGTTACATCAGGCACGAGCGTGAAC 3040 3050 3060

PHE LYS ASN GLY ASN ALA THR THR ALA THR ...  
TTCAAAACCGGCAATGCGGACCAACAGCGACC...  
3070 3080 3090...  
... VAL SER LYS ASP ASN GLY ASN ILE ASN VAL  
... GTAGCAAGATAATGGCAACATCAATGTC 3100 3110 3120

LYS TYR ASP VAL ASN VAL GLY ASP GLY LEU ...  
AAATACGATGTAAATGTGTGGTGACGGCTTG...  
3130 3140 3150...

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FIG.24P

... LYS ILE GLY ASP ASP LYS LYS ILE VAL ALA  
... AAGATTGGCCGATGACAAATAATCGTTGCA 3180  
... 3170

ASP THR THR THR LEU THR VAL THR GLY GLY ...  
GACACGACCACTTACTGTACACAGGTGGT... 3200  
... 3210

... LYS VAL SER VAL PRO ALA GLY ALA ASN SER  
... AAGGTGCTCTGTTCCCTGCTGGTGCTAATAGT 3240  
... 3220

VAL ASN ASN ASN LYS LYS LEU VAL ASN ALA ...  
GTTAATAACAATAAGAACTTGTATAATGCA... 3260  
... 3270

... GLU GLY LEU ALA THR ALA LEU ASN ASN LEU  
... GAGGGTTTAGCGACTGCTTTTAAACAACCTA 3300  
... 3280

SER TRP THR ALA LYS ALA ASP LYS TYR ALA ...  
AGCTGGACGGCAAAAGCCGATAATAATGCA... 3320  
... 3330

... ASP GLY GLU SER GLU GLY GLU THR ASP GLN  
... GATGGCGAGTCAGAGGGCGAAACCCGACCAA 3360  
... 3340

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FIG. 24Q

FIG.24Q

GLU VAL LYS ALA GLY ASP LYS VAL THR PHE ...  
GAAGTCAAGCAGGCGACAAAGTAACCTTT...  
3370 3380 3390...  
... LYS ALA GLY LYS ASN LEU LYS VAL LYS GLN  
... AAGCAGGCAAGAACTTAAAGTGAAACAG  
3400 3410 3420

SER GLU LYS ASP PHE THR TYR SER LEU GLN ...  
TCTGAAAGAGACTTTACTTTACTTACTGCA...  
3430 3440 3450...  
... ASP THR LEU THR GLY LEU THR SER ILE THR  
... GACACTTTAACAGGCTTACGAGCATTTACT  
3460 3470 3480

LEU GLY GLY THR ALA ASN GLY ARG ASN ASP ...  
TTAGGTGGTACAGCTAATGGCAGAAATGAT...  
3490 3500 3510...  
... THR GLY THR VAL ILE ASN LYS ASP GLY LEU  
... ACGGGAACCGTCATCAACAAAGACGGCTTA  
3520 3530 3540

THR ILE THR LEU ALA ASN GLY ALA ALA ...  
ACCATCAGCTGGCAAAATGGTGCTGCGGCA...  
3550 3560 3570...

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FIG. 24R

... GLY THR ASP ALA SER ASN GLY ASN THR ILE  
... GGCACAGATGCGTCTTAACGGAAACCATC 3600  
... 3580 3590

SER VAL THR LYS ASP GLY ILE SER ALA GLY ...  
AGTGTAACCAAGACGGCATTAGTGCGGT... 3620  
... 3630...  
... ASN LYS GLU ILE THR ASN VAL LYS SER ALA  
... AATAAGAAATTACCAATGTTAAGAGTGCT 3660  
... 3640 3650

LEU LYS THR TYR LYS ASP THR GLN ASN THR ...  
TTAAAACCTATAAAGATACTCAAAACACT... 3680  
... 3690...  
... ALA GLY ALA THR GLN PRO ALA ALA ASN THR  
... GCAGGTGCAACTCAACCTGCGGCTAATACA 3720  
... 3700 3710

ALA GLU VAL ALA LYS GLN ASP LEU VAL ASP ...  
GCTGAAGTAGCCAAACAAGACTTGGTTGAT... 3740  
... 3750...  
... LEU THR LYS PRO ALA THR GLY ALA ALA GLY  
... TTAACCTAACCTGCGGACAGGTGCAGCTGGA 3780  
... 3760 3770

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FIG.24S

ASN GLY ALA ASP ALA LYS ALA PRO ASP THR ...  
AATGGTGCAATGCAAAAGCTCCCGATACC...  
3790 3800 3810...  
... THR ALA ALA THR VAL GLY ASP LEU ARG GLY  
... ACAGCTGCAACCGTAGGCGACTTGCGTGGT 3830 3840

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LEU GLY TRP VAL LEU SER ALA LYS LYS THR ...  
TTGGGCTGGGTGCTTTTCAGCTAAGAAACT...  
3850 3860 3870...  
... ALA ASP GLU THR GLN ASP LYS GLU PHE HIS  
... GCAGATGAACAACAAGATTAAGAGTTCCAC 3890 3900

ALA ALA VAL LYS ASN ALA ASN GLU VAL GLU ...  
GCCGCCGTAAACAAACGCAAAATGAAGTTGAG...  
3910 3920 3930...  
... PHE VAL GLY LYS ASN GLY ALA THR VAL SER  
... TTCGTGGGTAAACACGGTGCAACCGTGCTT 3950 3960

ALA LYS THR ASP ASN ASN GLY LYS HIS THR ...  
GCAAAACTGATAACAAACGGAACAATACT...  
3970 3980 3990...

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FIG. 24T

FIG. 24T

... VAL THR ILE ASP VAL ALA GLU ALA LYS VAL  
... GTAACGATTGATGTTGCAGAGCCAAAGTT  
... 4000 4010 4020

GLY ASP GLY LEU LEU LYS ASP THR ASP GLY ...  
GGTGATGGTCTTGAAAGATACTGACGGC...  
4030 4040 4050...  
... LYS ILE LYS LEU LYS VAL ASP ASN THR ASP  
... AAGATTAAACTCAAGTAGATAATACAGAT  
... 4060 4070 4080

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GLY ASN ASN LEU LEU THR VAL ASP ALA THR ...  
GGGAATAATCTATTAAACCGTTGATGCAACA...  
4090 4100 4110...  
... LYS GLY ALA SER VAL ALA LYS GLY GLU PHE  
... AAGGTGCATCCGTTGCCCAAGGGCGAGTTT  
... 4120 4130 4140

ASN ALA VAL THR THR ASP ALA THR THR ALA ...  
AATGCCGTAACAACAGATGCAACTACAGCC...  
4150 4160 4170...  
... GLN GLY THR ASN ALA ASN GLU ARG GLY LYS  
... CAGGGCACAAATGCCCAATGAGCGCGGTAAA  
... 4180 4190 4200

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TABLE "SEQUENCE"

FIG.24U

VAL VAL VAL LYS GLY SER ASN GLY ALA THR ...  
GTGGTTGTCAAGGGTTCAAAATGGTGCAACT...  
4210 4220 4230...  
... ALA THR GLU THR ASP LYS LYS VAL ALA  
... GCTACCGAAACTGACAAAGAAAGTGGCA 4250 4260  
...

THR VAL GLY ASP VAL ALA LYS ALA ILE ASN ...  
ACTGTTGGCGACGTTGCTAAAGCGATTAAAC...  
4270 4280 4290...  
... ASP ALA ALA THR PHE VAL LYS VAL GLU ASN  
... GACGCACTTTCGTGAAAGTGGAAAT 4310 4320  
...

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ASP ASP SER ALA THR ILE ASP ASP SER PRO ...  
GACGACAGTGCTACGATTGATGATAGCCCA...  
4330 4340 4350...  
... THR ASP GLY ALA ASN ASP ALA LEU LYS  
... ACAGATGATGGCGCAATGATGCTCTCAA 4370 4380  
...

ALA GLY ASP THR LEU THR LEU LYS ALA GLY ...  
GCAGGCGACACCTTGACCTTAAGCGGGT...  
4390 4400 4410...

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FIG. 24V

FIG. 24V

... LYS ASN LEU LYS VAL LYS ARG ASP GLY LYS  
... AAAA CTTAAAGTTAAACGTTGATGGTAAA  
... 4420 4430 4440

ASN ILE THR PHE ALA LEU ALA ASN ASP LEU ...  
AATATTACTTTTGCCCTTGCGAACGACCTT...  
... 4450 4460 4470 ...  
... SER VAL LYS SER ALA THR VAL SER ASP LYS  
... AGTGTA AAAAGCGCAACCGTTAGCGATAAA  
... 4480 4490 4500

LEU SER LEU GLY THR ASN GLY ASN LYS VAL ...  
TTATCGCTTGGTACAAACGGCAATAAAGTC...  
... 4510 4520 4530 ...  
... ASN ILE THR SER ASP THR LYS GLY LEU ASN  
... AATATCAAGCGCACCAAAAGGCTTGAAAC  
... 4540 4550 4560

PHE ALA LYS ASP SER LYS THR GLY ASP ASP ...  
TTCGCTAAAGATAGTAAGACAGGCGATGAT...  
... 4570 4580 4590 ...  
... ALA ASN ILE HIS LEU ASN GLY ILE ALA SER  
... GCTAATAATTCACCTTAATAATGGCATTTGCTTCA  
... 4600 4610 4620

TTTGT" 24906666

FIG.24W

THR LEU THR ASP THR LEU LEU ASN SER GLY ...  
ACTTTAACTGATACATTTGTTAAATAGTGGT...  
4630 4640 4650...  
... ALA THR THR ASN LEU GLY GLY ASN GLY ILE  
... GCGACAAACCAATTAGGTGGTAAATGGTATT  
4660 4670 4680

THR ASP ASN GLU LYS LYS ARG ALA ALA SER ...  
ACTGATAACGAGAAATAACGCGCGGAGC...  
4690 4700 4710...  
... VAL LYS ASP VAL LEU ASN ALA GLY TRP ASN  
... GTTAAAGATGTCCTTGAAATGCCGGTGGGAAAT  
4720 4730 4740 136/204

VAL ARG GLY VAL LYS PRO ALA SER ALA ASN ...  
GTCGTGGTGTATAACCGGCATCTGCAAT...  
4750 4760 4770...  
... ASN GLN VAL GLU ASN ILE ASP PHE VAL ALA  
... AATCAAGTGGAGAAATATCGACTTTGTAGCA  
4780 4790 4800

THR TYR ASP THR VAL ASP PHE VAL SER GLY ...  
ACCTACGACACAGTGGAATTTGTAGTGGA...  
4810 4820 4830...



FIG.24X

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... ASP LYS ASP THR THR SER VAL THR VAL GLU  
... GATAAAGACACCAAGAGTGTAAGTTGAA 4860  
... 4840 4850

SER LYS ASP ASN GLY LYS ARG THR GLU VAL ...  
AGTAAAGATAATGGCAAGAGAACCGAAGTT... 4880  
... LYS ILE GLY ALA LYS THR SER VAL ILE LYS 4890...  
... AAAATCGGTGGCAAGACTTCTGTATTCAAA 4900 4910 4920  
... 4900

ASP HIS ASN GLY LYS LEU PHE THR GLY LYS ...  
GACCACAACGGCAAACTGTTTACAGGCAAA... 4930 4940 4950...  
... GLU LEU LYS ASP ALA ASN ASN GLY VAL  
... GAGCTGAAGGATGCTAACAAATAATGGCGTA 4960 4970 4980  
... 4960

THR VAL THR GLU THR ASP GLY LYS ASP GLU ...  
ACTGTTACCAGAAACCGACCGCAAGACGAG... 4990 5000 5010...  
... GLY ASN GLY LEU VAL THR ALA LYS ALA VAL  
... GGTAATGGTTTAGTGACTGCACAAAGCTGTG 5020 5030 5040  
... 5020

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SEQUENCE

FIG.24Y

ILE ASP ALA VAL ASN LYS ALA GLY TRP ARG ...  
ATTGATGCCGTTGAAATAAGGCTGGTTGGAGA...  
5050 5060 5070...  
... VAL LYS THR THR GLY ALA ASN GLY GLN ASN  
... GTTAAACAACAGGTGCTAATGGTCAGAAAT  
5080 5090 5100

ASP ASP PHE ALA THR VAL ALA SER GLY THR ...  
GATGACTTCGCAACTGTGTCAGGCACA...  
5110 5120 5130...  
... ASN VAL THR PHE ALA ASP GLY ASN GLY THR  
... AATGTAAACCTTTGCTGATGGTAAATGGCACACA  
5140 5150 5160

THR ALA GLU VAL THR LYS ALA ASN ASP GLY ...  
ACTGCCGAAGTAACATAAGCAACGACGGT...  
5170 5180 5190...  
... SER ILE THR VAL LYS TYR ASN VAL LYS VAL  
... AGTATTACTGTTAAATACAAATGTTAAAGTGT  
5200 5210 5220

ALA ASP GLY LEU LYS LEU ASP GLY ASP LYS ...  
GCTGATGGCTTAAAACTAGACGGCGATAA...  
5230 5240 5250...

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FIG. 24Z

FIG. 24Z

... ILE VAL ALA ASP THR THR VAL LEU THR VAL  
... ATCGTTGCAGACACGACCGTACTTACTGTG 5280  
... 5260 5270

ALA ASP GLY LYS VAL THR ALA PRO ASN ASN ...  
GCAGATGGTTAAGTTACAGCTCCGGAATAAT... 5300  
... GLY ASP GLY LYS LYS PHE VAL ASP ALA SER  
... GGCGATGGTTAAGAAATTTGTTGATGCCAAGT 5340  
... 5320 5330

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GLY LEU ALA ASP ALA LEU ASN LYS LEU SER ...  
GGTTAGCGGATGCGTTTAAATAATTAGC... 5360  
... TRP THR ALA THR ALA GLY LYS GLU GLY THR  
... TGGACGGCAACTGCTGGTTAAAGAAAGGCACT 5400  
... 5380 5390

GLY GLU VAL ASP PRO ALA ASN SER ALA GLY ...  
GGTGAAAGTTGATCCCTGCAATAATCAGCAGGG... 5420  
... GLN GLU VAL LYS ALA GLY ASP LYS VAL THR  
... CAGAGATCAAGCGGGCGGCAAGTAACC 5460  
... 5440 5450

FIG. 24A' 2999569

FIG. 24A'

PHE LYS ALA GLY ASP ASN LEU LYS ILE LYS ...  
T T T A A G C C G G C G A C A C C T G A A A T C A A A ...  
5470 5480 5490 ...  
... GIN SER GLY LYS ASP PHE THR TYR SER LEU  
... C A A G C G G C A A G A C T T T A C C T A C T C G C T G  
5500 5510 5520

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LYS LYS GLU LEU LYS ASP LEU THR SER VAL ...  
A A A A G A G C T G A A G A C C T G A C C A G C G T A ...  
5530 5540 5550 ...  
... GLU PHE LYS ASP ALA ASN GLY GLY THR GLY  
... G A G T T C A A A G A C G C A A C G G C G G T A C A G G C  
5560 5570 5580

SER GLU SER THR LYS ILE THR LYS ASP GLY ...  
A G T G A A G C A C C A A G A T T A C C A A A G A C G C ...  
5590 5600 5610 ...  
... LEU THR ILE THR PRO ALA ASN GLY ALA GLY  
... T T G A C C A T T A C G C C G G C A A C G G T G C G G T  
5620 5630 5640

ALA ALA GLY ALA ASN THR ALA ASN THR ILE ...  
G C G C A G G T G C A A C A C A C T G C A A C A C C A T ...  
5650 5660 5670 ...

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TABLET 20000000

FIG.24B'

... SER VAL THR LYS ASP GLY ILE SER ALA GLY  
... AGCGTAACCAAGATGGCATTAGCGGGT 5700  
... 5680

ASN LYS ALA VAL THR ASN VAL SER GLY ...  
AATAAGCAGTTACAAACGTTGTGAGCGGA... 5710  
5720  
... LEU LYS LYS PHE GLY ASP GLY HIS THR LEU  
... CTGAAGAAATTTGGTGATGGTCATACGTTG 5750  
... 5740 5760

ALA ASN GLY THR VAL ALA ASP PHE GLU LYS ...  
GCAATGGCACTGTGCTGATTTTGAAAG... 5770  
5780  
... HIS TYR ASP ASN ALA TYR LYS ASP LEU THR  
... CATTATGACCAATGCCCTATAAAGACTTGACC 5810  
... 5800 5820

ASN LEU ASP GLU LYS GLY ALA ASP ASN ...  
AATTGGATGAAAGAGCGCGGATAATAA... 5830  
5840  
... PRO THR VAL ALA ASP ASN THR ALA THR  
... CCGACTGTGCGGACAAATACCGCTGCAACC 5870  
... 5860 5880

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FIG. 24C

FIG. 24C

VAL GLY ASP LEU ARG GLY LEU GLY TRP VAL ...  
GTGGGCGATTGCGCGGCTTGGGCTGGGTC...  
5890 5900 5910...  
... ILE SER ALA ASP LYS THR THR GLY GLU PRO  
... ATTCTGCGGACAAACACACAGGCGAACCC  
5920 5930 5940

ASN GLN GLU TYR ASN ALA GLN VAL ARG ASN ...  
AATCAGGAATACACGCGCAAGTGCGTAAAC...  
5950 5960 5970...  
... ALA ASN GLU VAL LYS PHE LYS SER GLY ASN  
... GCCAATGAAGTGAAATTCAAGAGCGGCAAC  
5980 5990 6000

GLY ILE ASN VAL SER GLY LYS THR LEU ASN ...  
GGTATCAATGTTTCCGGTAAACATTGAAC...  
6010 6020 6030...  
... GLY THR ARG VAL ILE THR PHE GLU LEU ALA  
... GGTAACGCGGTGATTACCTTTGAAATTGGCT  
6040 6050 6060

LYS GLY GLU VAL VAL LYS SER ASN GLU PHE ...  
AAGGCGAAGTGGTAAATCGAATGAATT...  
6070 6080 6090...

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FIG. 24D

FIG. 24D

... THR VAL LYS ASN ALA ASP GLY SER GLU THR  
... ACCGTTAAGAAATGCCGATGGTTCGGAAACG 6120  
... 6100

ASN LEU VAL LYS VAL GLY ASP MET TYR ...  
AACTTGGTTTAAAGTTGGCGGATATGTATAC... 6140  
... 6130  
... SER LYS GLU ASP ILE ASP PRO ALA THR SER  
... AGCAAAGAGGATATTGACCCGGCAACCCAGT 6180  
... 6160

LYS PRO MET THR GLY LYS THR GLU LYS TYR ...  
AAACCGATGACAGGTAATAACTGAAAAATAT... 6200  
... 6190  
... LYS VAL GLU ASN GLY LYS VAL VAL SER ALA  
... AAGGTTGAAAAACGGCAAAAGTCGTTCTGCT 6240  
... 6220

ASN GLY SER LYS THR GLU VAL THR LEU THR ...  
AAGGCAGCAAGACCGAAGTTACCCCTAAC... 6260  
... 6250  
... ASN LYS GLY SER GLY TYR VAL THR GLY ASN  
... AACAAAGGTTCCGGCTATGTACAGGTAAAC 6300  
... 6280

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1116 P. 1116 " 2009000000

FIG.24E'

GIN VAL ALA ASP ALA ILE ALA LYS SER GLY ...  
CAAGTGGCTGATGCCGATTGCCGAAATCAGGC...  
6310  
... PHE GLU LEU GLY LEU ALA ASP ALA ALA GLU  
... TTTGAGCTTGGTTTGGCTGATGCCGCGCAGAA  
6340  
...

ALA GLU LYS ALA PHE ALA GLU SER ALA LYS ...  
GCTGAAAGAGCCCTTTGCCAGAAAGCGCAAA...  
6370  
... ASP LYS LYS GLU LEU SER LYS ASP LYS ALA GLU  
... GACAGCAATTGTCTTAAAGATTAAGCGGAA  
6400  
...

THR VAL ASN ALA HIS ASP LYS VAL ARG PHE ...  
ACTGTAAATGCCCAACGATATAAGTCCGTTT...  
6430  
... ALA ASN GLY LEU ASN THR LYS VAL SER ALA  
... GCTAATGGTTTAAATACCAAGTGAAGCGCG  
6460  
...

ALA THR VAL GLU SER THR ASP ALA ASN GLY ...  
GCAACGGTGGAAAGCACTGATGCCAAACGGC...  
6490  
6510...

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6420

6410

6480

6470

6460

6510...

6490



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FIG. 24F' 28E9E560

FIG. 24F'

... ASP LYS VAL THR THR PHE VAL LYS THR  
... GATAAAGTGACCAACCTTTGTGAAACC 6540  
... 6520 6530

ASP VAL GLU LEU PRO LEU THR GIN ILE TYR ...  
GATGTGGAATTGCTTTTACGCAATCTAC... 6550  
... 6560 6570...

... ASN THR ASP ALA ASN GLY ASN LYS ILE VAL  
... AATACCGATGCCAAACGGTAATAAGATCGTT 6600  
... 6580 6590

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LYS LYS ALA ASP GLY LYS TRP TYR GLU LEU ...  
AAAAAGCTGACGGGAAAATGGTATGAAC TG... 6610  
... 6620 6630...

... ASN ALA ASP GLY THR ALA SER ASN LYS GLU  
... AATGCTGATGGTACGGCGAGTAACAAGAA 6660  
... 6640 6650

VAL THR LEU GLY ASN VAL ASP ALA ASN GLY ...  
GTGACACTTGTTAACGTGATGCAACGGT... 6670  
... 6680 6690...

... LYS LYS VAL VAL LYS VAL THR GLU ASN GLY  
... AAGAAAGTTGTGAAGTAACCGGAAATGGT 6720  
... 6700 6710

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PCT/CA00/00289

TABLET 2995660

FIG.24G'

ALA ASP LYS TRP TYR THR ASN ALA ASP ...  
GCGGATAAGTGGTATTACACCAATGCTGAC...  
6730 6750...  
... GLY ALA ALA ASP LYS THR LYS GLY GLU VAL  
... GGTGCTGCGGATATAAACCAAGGCGAAGTG  
6760 6770 6780

SER ASN ASP LYS VAL SER THR ASP GLU LYS ...  
AGCAATGATAAAGTTTCTTACCGATGAA...  
6790 6810...  
... HIS VAL VAL ARG LEU ASP PRO ASN ASN GLN  
... CACGTTGTCGCGCTTGATCCGAACAATCAA  
6820 6830 6840

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SER ASN GLY LYS GLY VAL VAL ILE ASP ASN ...  
TCGAACGGCAAGGCGTGGTCAATTGACAT...  
6850 6870...  
... VAL ALA ASN GLY GLU ILE SER ALA THR SER  
... GTGGCTAATGGCGGAATTTCTGCCACTTCC  
6880 6890 6900

THR ASP ALA ILE ASN GLY SER GIN LEU TYR ...  
ACCGATGCGATTAAACGGAAGTCAGTTGTAT...  
6910 6930...

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FIG.24H'

FOOTNOTES

... ALA VAL ALA LYS GLY VAL THR ASN LEU ALA  
... GCCGTGGCAAAAGGGGTAACAAACCTTGCT  
... 6940 6950 6960

GLY GLN VAL ASN LEU GLU GLY LYS VAL ...  
GGACAAGTGATAATCTTGAGGGCAAAAGTG...  
6970 6980 6990...  
... ASN LYS VAL GLY LYS ARG ALA ASP ALA GLY  
... AATAAGTGGGCAACCGTGCGAGATGCAGGT  
... 7000 7010 7020

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THR ALA SER ALA LEU ALA ALA SER GLN LEU ...  
ACAGCAAGTGCAATTAGCGGCTTCACAGTTA...  
7030 7040 7050...  
... PRO GLN ALA THR MET PRO GLY LYS SER MET  
... CCACAGCCACTATGCCAGGTAAATCAATG  
... 7060 7070 7080

VAL ALA ILE ALA GLY SER TYR GLN GLY ...  
GTTGCTATTGCGGGAAGTAGTTATCAAGGT...  
7090 7100 7110...  
... GLN ASN GLY LEU ALA ILE GLY VAL SER ARG  
... CAAATGGTTTAGCTATCGGGGTATCAAGA  
... 7120 7130 7140

FIG. 24I'

THR GLY VAL ALA ALA GLY VAL GLY TYR GLN ...  
A C A G G C G T T G C A G C A G G T G T T G G T T A C C A G ...  
7210 7220 \*\*\* TRP ... T G G T A A T A G A A T T C C G G A T C C G C  
7230... 7240 7250

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FIG.25A

NTHi strain 12 hia locus

TTCTTTT TTTCTTT

TYR TYR HIS TRP \*\*\* PRO THR PRO ...  
GAATTCTATTACCACTGGGTAAACCAACACCT ...  
10 20 30 ...

... ALA ALA THR PRO GLU THR ALA GIN GIN ILE  
...GCTGCAACGCCAGAAACAGCACAAACAATT  
... 40 50 60

HIS TRP LEU HIS GIN PHE THR LYS ALA ARG ...  
CACTGGCTACATCAATTACCAAGCTCGC ...  
70 80 90 ...

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... ILE GIN TRP ARG LYS THR HIS SER LEU PHE  
...ATTCAATGGCGCAAAACCCATTCTTATTCT  
... 100 110 120

PHE LYS GLU LYS PRO ASP TYR ALA PHE VAL ...  
TTTAAAGAAATAACCCGATATATGCTTTGTG ...  
130 140 150 ...

... LEU ALA GLU ASN GLY LYS VAL GIN GLU ILE  
...CTGGCAGAAACCGGCAAGTGCAAGAAATC  
... 160 170 180

LYS ALA GLU TYR ARG ARG ILE ALA ASN GIN ...  
AAGCAGAAATATCGCCGCAATGCCAAATCAA ...  
190 200 210 ...

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FIG. 25B

FIG. 25B

... ILE VAL GLU GLU ALA MET ILE ILE ALA ASN  
...ATTGGGAAGAGCAATGATTATTGCCAAC  
... 220 230 240

ILE CYS ALA ALA GLN PHE LEU HIS GLU GLN ...  
ATCTGCGCGCCCAATTTTTACACGACAG ...  
250 260 270 ...  
... ALA LYS THR GLY ILE PHE ASN ALA HIS SER  
...GCAAAACAGGCAATTTCAACGCCACAGC  
... 280 290 300

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GLY PHE ASP LYS LYS TYR LEU GLU ASN ALA ...  
GGTTTGTATAAATACTTAGAAATGCG ...  
310 320 330 ...  
... HIS HIS PHE LEU MET ALA ASN LEU ALA ASN  
... 6431.SL ( ...  
...CACCAATTTCTTAATGGCAATTTAGCCAAT  
... 340 350 360

GLU GLN ASN GLN THR GLU LEU ALA GLU ARG ...  
GAACAATACTCAACTGAACCTGGCAGAACGT ...  
370 380 390 ...  
... TYR SER VAL GLU ASN LEU ALA THR LEU ASN  
...TATTCAGTAGAAACCTTAGCAACCTTAAC  
... 400 410 420

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

FIG. 25C

GLY	TYR	CYS	GLN	MET	ARG	HIS	ASP	ILE	GLU	...
GGC	TAT	TGC	CAA	AAT	GCG	TCA	CGA	TATT	GAA	...
									440	450 ...
									430	...
									... PRO	ILE GLU SER ASP TYR LEU GLU LEU ARG
									...CCC	ATCGAAGCGATTATTAGAACTGCGT
									460	470
									480	

LEU ARG ARG ARG TYR LEU LEU THR PHE ALA GLU PHE ...  
T T A C G C G T A T T A C T T T C G C G A A T T ...  
490  
... LYS SER GLU LEU ALA PRO HIS PHE GLY LEU  
... A A A T C A G A A T T A G C A C C G C A C T T T G G T C T T  
500 510 ... 520 530 540

GLY LEU GLU GLY TYR ALA THR TRP THR SER ...  
 GGT TAGAGGCTATGCCACTTGGACATCG ...  
 550  
 ... PRO ILE ARG LYS TYR SER ASP MET VAL ASN  
 ...CCCATCCGCAATAATTCAGATA TGGTTAAT  
 580 590 600

HIS ARG LEU ILE LYS ALA VAL LEU ALA LYS ...  
 C A T C G C T T A A T C A A A G C C G T G C T G G C A A A ...  
 610 620 630 ...

FIG. 25D

Case	Age	Sex	Duration	Site	Pathology	Response	Survival
1	65	M	10 years	Rectum	Adenocarcinoma	Complete	5 years
2	58	F	5 years	Colon	Adenocarcinoma	Partial	3 years
3	72	M	15 years	Rectum	Adenocarcinoma	Complete	10 years
4	60	F	8 years	Colon	Adenocarcinoma	Partial	4 years
5	68	M	12 years	Rectum	Adenocarcinoma	Complete	6 years
6	55	F	7 years	Colon	Adenocarcinoma	Partial	3 years
7	70	M	18 years	Rectum	Adenocarcinoma	Complete	12 years
8	62	F	9 years	Colon	Adenocarcinoma	Partial	4 years
9	66	M	14 years	Rectum	Adenocarcinoma	Complete	7 years
10	59	F	6 years	Colon	Adenocarcinoma	Partial	3 years

... GLN PRO TYR GLU LYS PRO GIN ASN ASP VAL  
...  
...CAGCCTTATGAATAAACCAACAATA GACGTG  
... 640 650

LEU ALA ARG LEU GIN SER ARG ARG GIN ...  
6432.SL (  
TTGGCACGTTTGCAAGAGTCTCGCCGCCAA ...  
670 680 690 ...  
... ASN ARG LEU VAL GLU ARG ASP ILE ALA ASP  
...  
...ATCGCCTAGTGGAACGTGATATTGCCGATT  
... 700 710 720

TRP LEU TYR CYS ARG TYR LEU ALA ASP LYS ...  
TGGCTATAATGCGGTTATCTTGCTGACAAA ...  
730 740 750 ...  
... VAL ALA GLU ASN VAL GLU PHE ASN ALA GLU  
...GTGGCTGAAAAATGTGGAATTTAATGCAGAA  
... 760 770 780

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FIG.25E

SEQUENCE

... VAL GIN LEU LEU GLU ASN GLY ALA SER LEU  
...GTACAACTGCTCGAAATAATGGTGCAATCGCTA 840  
... 820

PHE ILE PRO ALA ALA THR LEU HIS ASN ASN ...  
TTTATTCTCTGCGCCACGTTGCAACAAC... 850  
... 860

... LYS GLU GLU ILE GIN LEU ASN PRO ASP GLU  
...AAGAAGAAATACAGCTAAACCCCTGACGAA 900  
... 880

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LEU ALA LEU TYR ILE LYS GLY GLU ARG THR ...  
CTCGCCCTCTATATAAAGGCGAACGCACT... 910  
... 920

... TYR LYS ILE GLY ASP ILE VAL LYS VAL LYS  
...TACAAATAAGCGGACATTTGTGAAAGTGAA 960  
... 940

LEU THR GLU VAL LYS GLU ALA THR ARG SER ...  
CTCACAGAGTGAAAGAGCAACTCGCAGT... 970  
... 980

... ILE VAL GLY GLU ILE LEU GIN \*\*\* LEU PRO  
...ATTGTGGGCGAAATACTTCAATAAATTGCC 1020  
... 1000

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FIG.25F

PHE GIN TYR VAL THR GLU ASP GLY LYS THR...  
GTTCCAAATATGTTACGGAGACGGCAAAC...  
1030 1040 1050 ...  
... VAL VAL LYS VAL GLY ASN GLU TYR TYR GLU  
...CGTTGTGAAGTGGGCAATGAGTATTACGA  
1060 1070 1080

ALA LYS GIN ASP GLY SER ALA ASP MET ASP...  
AGCCAAGCAAGACGGTTCGGCGGATATGGA...

( 6295.SL

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1090 1100 1110 ...  
... LYS LYS VAL LYS ASN GLY GLU LEU VAL LYS  
...TAAAGTCAAAATGGCGAGCTGGTGAA  
... 1120 1130 1140

THR LYS VAL LYS LEU VAL SER ALA ASN GLY...  
AACTAAGTGAAATTGGTATCGGCAACGG...  
1150 1160 1170 ...  
... THR ASN PRO VAL LYS ILE SER ASN VAL ALA  
...TACAAATCCGGTGAAATCAGCAATGTTGC  
1180 1190 1200

GLU GLY THR GLU ASP THR ASP ALA VAL SER...  
GGAAGGCACGGAGATACCGATCGGTCAG...  
1210 1220 1230 ...

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FIG.25G

... PHE LYS GLN LEU LYS ALA LEU GIN ASN LYS  
...CTTAAGCAGTTGAAAGCCCTTGCAAAACAA 1260  
... 1240 1250

GLN VAL THR LEU SER ALA SER ASN ALA TYR...  
ACAGGTTACGTTTAGCGCGGAGCAATGCTTA ... 1270  
... 1280  
... ALA ASN GLY GLY SER ASP ALA ASP VAL GLY  
...TGCCCAATGCGCGGTAGCGATGCCGACGTCGG 1320  
... 1300 1310

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LYS VAL THR GIN THR LEU SER ASN GLY LEU...  
CAGGTAACCTCAAACTTTTAGCAATGGTTT ... 1330  
... 1340  
... ASN PHE LYS PHE LYS SER THR ASP GLY GLU  
...GAATTTTAAATTAAATCCACAGACGGCGA 1380  
... 1360 1370

LEU LEU ASN ILE LYS ALA ASP LYS ASP THR...  
GTTGTTGAACATCAAGCAGACAGGACAC ... 1390  
... 1400  
... VAL THR ILE THR ARG ALA SER GLY ALA ASN  
...GGTTACCAATTACCGCGGCAAGCGGTGCGAA 1440  
... 1420 1430

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FIG. 25H

FIG. 25H

GLY ALA ALA THR ASP ALA ASP LYS ILE...  
TGGTGGCGGCGGACTGATGCCGACAAGAT...  
1450 1460 1470 ...  
... LYS VAL ALA SER ASP GLY ILE SER ALA GLY  
...TAAAGTGGCTTCAGACGGCATTAGCGCGGG  
1480 1490 1500

ASN LYS ALA VAL LYS ASN VAL ALA GLY...  
TAATAAGCAGTTATAAACGTCGCCGCGAGG...  
1510 1520 1530 ...  
... GLU ILE SER ALA THR SER THR ASP ALA ILE  
...CGAAATTTCGCCCACTTCCACCGATGCGGAT  
... ( 6271.SL 1550 1560

ASN GLY SER GLN LEU TYR ALA VAL ALA LYS...  
TAACGGCAGTCAGTTGTATGCCGTGGCAAA...  
1570 1580 1590 ...  
... GLY VAL THR ASN LEU ALA GLY GLN VAL ASN  
...GGGGGTAAACAACCTTGCTGGACAAGTGAA  
1600 1610 1620

LYS VAL GLY LYS ARG ALA ASP ALA GLY THR...  
TAAGTGGGCAACCGTGCAAGATGCAAGGTAC...  
1630 1640 1650 ...

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FIG. 251

FIG.251

... ALA SER ALA LEU ALA ALA SER GIN LEU PRO  
...AGCAAGTGCAATTAGCGGCTTCACAGTTACC  
... 1660 1670 1680

GLN ALA SER MET PRO GLY LYS SER MET VAL...  
ACAAGCCCTCTATGCCCCGTAAATCAATGGT...  
1690 1700 1710 ...  
... SER ILE ALA GLY SER TYR GIN GLY GIN  
...TCTATTGCGGGAAGTAGTTATCAAGGTCA  
... 1720 1730 1740

SER GLY LEU ALA ILE GLY VAL SER ARG ILE...  
AAGTGGTTTAGCTATCGGGGTATCAAGAAAT...  
1750 1760 1770 ...  
... SER ASP ASN GLY LYS LEU ILE ILE ARG LEU  
...TCCGATAATGGCAAAATTGATTATTGCGCTT  
... 1780 1790 1800

SER GLY THR THR ASN SER GIN GLY LYS THR...  
GTCAGGCCACAACCAATAGCCCAAGGTAAAC...  
1810 1820 1830 ...  
... GLY VAL ALA ALA GLY VAL GLY TYR GIN TRP  
...AGGCGTTGCAAGCAGGTGTTGGTTACCAAGTG  
... 1840 1850 1860

\*\*\* \*\*

GTAATAGAAATTC  
1870

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# FIG.26A

ATG AAC AAA ATT TTT AAC GGT ATT TGG AAT GGT GGT ACT CAA ACT TGG Met Asn Lys Ile Phe Asn Val Ile Trp Asn Val Val Thr Gln Thr Trp 2130 2135 2140	48
GGT GTC GTA TCT GAA CTC ACT GGC ACC CAC ACC AAA TGC GGC TCC GGC Val Val Val Ser Glu Leu Thr Arg Thr His Thr Lys Cys Ala Ser Ala 2145 2150 2155	96
ACC GTG GCG GTT GGC GTA TTG GCA ACC CTG TTG TCC GCA ACG GGT GAG Thr Val Ala Val Ala Val Leu Ala Thr Leu Ser Ala Thr Val Glu 2160 2165 2170 2175	144
GCG AAC AAC AAT ACT CCT GGT ACT AAT AAT AAT TTT AAG GGT TAT GGC GAT Ala Asn Asn Asn Thr Pro Val Thr Asn Lys Leu Lys Ala Tyr Gly Asp 2180 2185 2190	192
GCG AAT TTT AAT TTC ACT AAT AAT TCG ATA GCA GAT GCA GAA AAA CAA Ala Asn Phe Asn Phe Thr Asn Asn Ser Ile Ala Asp Ala Glu Lys Gln 2195 2200 2205	240
GGT CAA GAG CCT TAT AAA GGT TTA TTA AAT CTA AAT GAA AAA AAT GCG Val Gln Glu Ala Tyr Lys Gly Leu Leu Asn Leu Asn Glu Lys Asn Ala 2210 2215 2220	288

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FIG. 26B

FIG. 26B

AGT GAT AAA CTG TTG GTG GAG GAC AAT ACT GCG GCG ACC GTA GGC AAT Ser Asp Lys Leu Leu Val Glu Asp Asn Thr Ala Ala Thr Val Gly Asn 2225 2230 2235	336
TTG CGT AAA TTG GGC TGG GTA TTG TCT AGC AAA AAC GGC ACA AGG AAC Leu Arg Lys Leu Gly Trp Val Leu Ser Ser Lys Asn Gly Thr Arg Asn 2240 2245 2250 2255	384
GAG AAA AGC CAA CAA GTC AAA CAT CCG GAT GAA GTG TTG TTT GAA GGC Glu Lys Ser Gln Gln Val Lys His Ala Asp Glu Val Leu Phe Glu Gly 2260 2265 2270	432
AAA GGC GGT GTG CAG GTT ACT TCC ACC TCT GAA AAC GGC AAA CAC ACC Lys Gly Gly Val Gln Val Thr Ser Thr Ser Glu Asn Gly Lys His Thr 2275 2280 2285	480
ATT ACC TTT GCT TTA GCG AAA GAC CTT GGT GTG AAA ACT GCG ACT GTG Ile Thr Phe Ala Leu Ala Lys Asp Leu Gly Val Lys Thr Ala Thr Val 2290 2295 2300	528
AGT GAT ACC TTA ACG ATT GGC GGT GGT GCT GCA GGT GCT ACA ACA Ser Asp Thr Leu Thr Ile Gly Gly Gly Ala Ala Gly Ala Thr Thr 2305 2310 2315	576

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FIG.26C

ACA CCG AAA GTG AAT GTA ACT AGT ACA ACT GAT GGC TTG AAG TTC GCT Thr Pro Lys Val Asn Val Thr Ser Thr Thr Asp Gly Leu Lys Phe Ala 2320 2325 2330 2335	624
AAA GAT GCT GCG GGT GCT AAT GGC GAT ACT ACG GIT CAC TTG AAT GGT Lys Asp Ala Ala Gly Ala Asn Gly Asp Thr Thr Val His Leu Asn Gly 2340 2345 2350	672
ATT GGT TCA ACC TTG ACA GAC ACG CTT GTG GGT TCT CCT GCT ACT CAT Ile Gly Ser Thr Leu Thr Asp Thr Leu Val Gly Ser Pro Ala Thr His 2355 2360 2365	720
ATT GAC CGA CGA GAT CAA AGT ACG CAT TAC ACT CGT GCA GCA AGT ATC Ile Asp Gly Gly Asp Gln Ser Thr His Tyr Thr Arg Ala Ala Ser Ile 2370 2375 2380	768
AAG GAT GTC TTG AAT CCG GGT TCG AAT ATC AAG GGT GIT AAA GCT GCG Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys Ala Gly 2385 2390 2395	816
TCA ACA ACT GGT CAA TCA GAA AAT GTC GAT TTT GIT CAT ACT TAC GAT Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val His Thr Tyr Asp 2400 2405 2410 2415	864

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FIG.26D

ACT GTT GAG TTC TTG AGT GCG GAT ACA GAG ACC ACG ACT GTT ACT GTA Thr Val Glu Phe Leu Ser Ala Asp Thr Glu Thr Thr Val Thr Val	912
2420 2425 2430	
GAT AGC AAA GAA AAC CCG AAG ACA ACC GAA GTT AAA ATC GGT GCG AAG Asp Ser Lys Glu Asn Gly Lys Arg Thr Glu Val Lys Ile Gly Ala Lys	960
2435 2440 2445	
ACT TCT GTT ATC AAA GAA AAA GAC GGT AAG TTA TTT ACT CGA AAA GCT Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Phe Thr Thr Gly Lys Ala	1008
2450 2455 2460	
AAC AAA GAG ACA AAT AAA GTT GAT GGT GCT AAC GCG ACT GAA GAT GCA Asn Lys Glu Thr Asn Lys Val Asp Gly Ala Asn Ala Thr Glu Asp Ala	1056
2465 2470 2475	
GAC GAA GCG AAA GGC TTA GTG ACT GCG AAA GAT GTG ATT GAC GCA GTG Asp Glu Gly Lys Gly Leu Val Thr Ala Lys Asp Val Ile Asp Ala Val	1104
2480 2485 2490 2495	
AAT AAG ACT GGT TCG AGA ATT AAA ACA ACC GAT GCT AAT GGT CAA AAT Asn Lys Thr Gly Trp Arg Ile Lys Thr Thr Asp Ala Asn Gly Gln Asn	1152
2500 2505 2510	

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FIG. 26E

FIG. 26E

GCC GAC TTC GCA ACT GTT GCA TCA GGC ACA AAT GTA ACC TTT GCT AGT Gly Asp Phe Ala Thr Val Ala Ser Gly Thr Asn Val Thr Phe Ala Ser 2515 2520 2525	1200
GGT AAT GGT ACA ACT GCG ACT GTA ACT AAT GGC ACC GAT GGT ATT ACC Gly Asn Gly Thr Thr Ala Thr Val Thr Asn Gly Thr Asp Gly Ile Thr 2530 2535 2540	1248
GTT AAG TAT GAT GCG AAA GTT GCG GAC GGC TTA AAA CTA GAT GGC GAT Val Lys Tyr Asp Ala Lys Val Gly Asp Gly Leu Lys Leu Asp Gly Asp 2545 2550 2555	1296
AAA ATC GCT GCA GAT ACG ACC GCA CTT ACT GTG AAT GAT GGT AAG AAC Lys Ile Ala Ala Asp Thr Thr Ala Leu Thr Val Asn Asp Gly Lys Asn 2560 2565 2570 2575	1344
GCT AAT AAT CCG AAA GGT AAA GTG GCT GAT GTT GCT TCA ACT GAC GAG Ala Asn Asn Pro Lys Gly Lys Val Ala Asp Val Ala Ser Thr Asp Glu 2580 2585 2590	1392
AAG AAA TTG GTT ACA GCA AAA GGT TTA GTA ACA GCC TTA AAC AGT CTA Lys Lys Leu Val Thr Ala Lys Gly Leu Val Thr Ala Leu Asn Ser Leu 2595 2600 2605	1440

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FIG.26F

ACC TGG ACT ACA ACT GCT GCT GAG GCG GAC GGT GGT ACG CTT GAT GGA	1488
Ser Trp Thr Thr Ala Ala Glu Ala Asp Gly Gly Thr Leu Asp Gly	2610 2615 2620
AAT GCA AGT GAG CAA GAA GTT AAA GCG GCG GAT AAA GTA ACC TTT AAA	1536
Asn Ala Ser Glu Gln Glu Val Lys Ala Glu Asp Lys Val Thr Phe Lys	2625 2630 2635
GCA GCG AAG AAC TTA AAA GTG AAA CAA GAG GGT GCG AAC TTT ACT TAT	1584
Ala Gly Lys Asn Leu Lys Val Lys Gln Glu Gly Ala Asn Phe Thr Tyr	2640 2645 2650 2655
TCA CTG CAA GAT GCT TTA ACA GCG TTA ACG AGC ATT ACT TTA GGT ACA	1632
Ser Leu Gln Asp Ala Leu Thr Gly Leu Thr Ser Ile Thr Leu Gly Thr	2660 2665 2670
GGA AAT AAT GGT GCG AAA ACT GAA ATC AAC AAA GAC GCG TTA ACC ATC	1680
Gly Asn Asn Gly Ala Lys Thr Glu Ile Asn Lys Asp Gly Leu Thr Ile	2675 2680 2685
ACA CCA GCA AAT GGT GCG GGT GCA AAT AAT GCA AAC ACC ATC AGC GTA	1728
Thr Pro Ala Asn Gly Ala Gly Ala Asn Asn Ala Asn Thr Ile Ser Val	2690 2695 2700

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# FIG.26G

ACC AAA GAC GGC ATT AGT GCG GGC CAG TCG GGT AAA AAC GGT GTC	1776
Thr Lys Asp Gly Ile Ser Ala Gly Gly Ser Val Lys Asn Val Val	
2705 2710 2715	
ACC GGA CTG AAG AAA TTT GGT GAT GCG AAT TTC GAT CCG CTG ACT AGC	1824
Ser Gly Leu Lys Lys Phe Gly Asp Ala Asn Phe Asp Pro Leu Thr Ser	
2720 2725 2730 2735	
TCC GGC GAC AAC TTA ACG AAA CAA AAT GAC GAT GGC TAT AAA GGC TTG	1872
Ser Ala Asp Asn Leu Thr Lys Gln Asn Asp Ala Tyr Lys Gly Leu	
2740 2745 2750	
ACC AAT TTG GAT GAA AAA GGT ACA GAC AAG CAA ACT OCA GGT GTC GGC	1920
Thr Asn Leu Asp Glu Lys Gly Thr Asp Lys Gln Thr Pro Val Val Ala	
2755 2760 2765	
GAC AAT ACC GGC GCA ACC GTG GGC GAT TTG CCG GGC TTG GGC TCG GTC	1968
Asp Asn Thr Ala Ala Thr Val Gly Asp Leu Arg Gly Leu Gly Trp Val	
2770 2775 2780	
ATT TCT GCG GAC AAA ACC ACA GGC GGC TCA ACG GAA TAT CAC GAT CAA	2016
Ile Ser Ala Asp Lys Thr Thr Gly Gly Ser Thr Glu Tyr His Asp Gln	
2785 2790 2795	

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FIG. 26H

FIG. 26H

GTT CCG AAT GCG AAC GAA GIG AAA TTC AAA AGC GGC AAC GGT ATC AAT Val Arg Asn Ala Asn Glu Val Lys Phe Lys Ser Gly Asn Gly Ile Asn 2800 2805 2810 2815	2064
GTT TCC GGT AAA ACG GTC AAC GGT AGG GGT GAA ATT ACT TTT GAA TTG Val Ser Gly Lys Thr Val Asn Gly Arg Arg Glu Ile Thr Phe Glu Leu 2820 2825 2830	2112
GCT AAA GGT GAA GIG GTT AAA TCG AAT GAA TTT ACC GTC AAA GAA ACC Ala Lys Gly Glu Val Val Lys Ser Asn Glu Phe Thr Val Lys Glu Thr 2835 2840 2845	2160
AAT GGA AAG GAA ACG ACC CTG GTT AAA GTT GGC GAT AAA TAT TAC AGC Asn Gly Lys Glu Thr Ser Leu Val Lys Val Gly Asp Lys Tyr Tyr Ser 2850 2855 2860	2208
AAA GAG GAT ATT GAC TTA ACA ACA GGT CAG CCT AAA TTA AAA GAT GGC Lys Glu Asp Ile Asp Leu Thr Thr Gly Gln Pro Lys Leu Lys Asp Gly 2865 2870 2875	2256
AAT ACA GTT GCT GCG AAA TAT CAA GAT AAA GGT GGC AAA GTC GTT TCT Asn Thr Val Ala Ala Lys Tyr Gln Asp Lys Gly Gly Lys Val Val Ser 2880 2885 2890 2895	2304

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FIG.261

GTA ACG GAT AAT ACT GAA GCT ACC ATA ACC AAC AAA GGT TCT GGC TAT Val Thr Asp Asn Thr Glu Ala Thr Ile Thr Asn Lys Gly Ser Gly Tyr 2900 2905 2910	2352
GTA ACA GGT AAC CAA GTG CCA GAT GCG ATT CCG AAA TCA GGC TTT GAG Val Thr Gly Asn Gln Val Ala Asp Ala Ile Ala Lys Ser Gly Phe Glu 2915 2920 2925	2400
CTT GGC TTG GCT GAT GAA GCT GAT GCG AAA CCG GCG TTT GAT GAT AAG Leu Gly Leu Ala Asp Glu Ala Asp Ala Lys Arg Ala Phe Asp Asp Lys 2930 2935 2940	2448
ACA AAA GGC TTA TCT GCT GGT ACA ACG GAA ATT GTA AAT GGC CAC GAT Thr Lys Ala Leu Ser Ala Gly Thr Thr Glu Ile Val Asn Ala His Asp 2945 2950 2955	2496
AAA GTC CGT TTT GCT AAT GGT TTA AAT ACC AAA GTG ACG GCG GCA ACG Lys Val Arg Phe Ala Asn Gly Leu Asn Thr Lys Val Ser Ala Ala Thr 2960 2965 2970 2975	2544
GTG GAA ACG ACC GAT GCA AAC GGC GAT AAA GTG ACC ACA ACC TTT GTG Val Glu Ser Thr Asp Ala Asn Gly Asp Lys Val Thr Thr Phe Val 2980 2985 2990	2592

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106121 29090560

# FIG.26J

AAA ACC GAT GTG GAA TTG OCT TTA ACG CAA ATC TAC AAT ACC GAT GCA Lys Thr Asp Val Glu Leu Pro Leu Thr Gln Ile Tyr Asn Thr Asp Ala 2995 3000 3005	2640
AAC GGT AAG AAA ATC ACT AAA GTT GTC AAA GAT GGG CAA ACT AAA TGG Asn Gly Lys Lys Ile Thr Lys Val Val Lys Asp Gly Gln Thr Lys Trp 3010 3015 3020	2688
TAT GAA CTG AAT GCT GAC GGT ACG GCT GAT ATG ACC AAA GAA GTT ACC Tyr Glu Leu Asn Ala Asp Gly Thr Ala Asp Met Thr Lys Glu Val Thr 3025 3030 3035	2736
CTC GGT AAC GTG GAT TCA GAC GGC AAG AAA GTT GTG AAA GAC AAC GAT Leu Gly Asn Val Asp Ser Asp Gly Lys Lys Val Val Lys Asp Asn Asp 3040 3045 3050 3055	2784
GGC AAG TGG TAT CAC GCC AAA OCT GAC GGT ACT GCG GAT AAA ACC AAA Gly Lys Trp Tyr His Ala Lys Ala Asp Gly Thr Ala Asp Lys Thr Lys 3060 3065 3070	2832
GGC GAA GTG ACG AAT GAT AAA GTT TCT ACC GAT GAA AAA CAC GTT GTC Gly Glu Val Ser Asn Asp Lys Val Ser Thr Asp Glu Lys His Val Val 3075 3080 3085	2880

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FIG. 26K

FIG. 26K

AGC CTT GAT CCA AAT GAT CAA TCA AAA GGT AAA GGT GTC GTG ATT GAC Ser Leu Asp Pro Asn Asp Gln Ser Lys Gly Lys Gly Val Val Ile Asp 3090 3095 3100	2928
AAT GTG GCT AAT GGC GAT AAT TCT GCC ACT TCC ACC GAT GCG ATT AAC Asn Val Ala Asn Gly Asp Ile Ser Ala Thr Ser Thr Asp Ala Ile Asn 3105 3110 3115	2976
GCA AGT CAG TTG TAT GCT GTG GCA AAA GCG GTA ACA AAC CTT GCT GGA Gly Ser Gln Leu Tyr Ala Val Ala Lys Gly Val Thr Asn Leu Ala Gly 3120 3125 3130 3135	3024
CAA GTG AAT AAT CTT CAG GGC AAA GTG AAT AAA GTG GGC AAA CGT GCA Gln Val Asn Asn Leu Glu Gly Lys Val Asn Lys Val Gly Lys Arg Ala 3140 3145 3150	3072
GAT CCA GGT ACA GCA AGT GCA TTA GCG GCT TCA CAG TTA CCA CAA GCC Asp Ala Gly Thr Ala Ser Ala Leu Ala Ala Ser Gln Leu Pro Gln Ala 3155 3160 3165	3120
ACT ATG CCA GGT AAA TCA ATG GTT GCT ATT GCG GCA AGT AGT TAT CAA Thr Met Pro Gly Lys Ser Met Val Ala Ile Ala Gly Ser Ser Tyr Gln 3170 3175 3180	3168



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FIG. 26L

FIG.26L

GGT CAA AAT	GGT TTA GCT ATC GCG GTA TCA AGA ATT TCC GAT AAT GGC	3216
Gly Gln Asn Gly Leu Ala Ile Gly Val Ser Arg Ile Ser Asp Asn Gly		
3185	3190	
AAA GTG ATT AIT CCG TTG TCA GCG ACA ACC AAT AGT CAA GGT AAA ACA		3264
Lys Val Ile Ile Arg Leu Ser Gly Thr Thr Asn Ser Gln Gly Lys Thr		
3200	3205	
GGC GTT CCA CCA GGT GGT TAC CAG TGG		3294
Gly Val Ala Ala Gly Val Gly Tyr Gln Trp		
	3220	
	3225	
	3210	
	3215	

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FIG.27A

Alignment of NIH strain 12 5' ORF with HI1733 from H. influenzae strain Rd

X	10	20	30	40	50	60	70
PTPAATPETAQQIHLHQFTKARIQMRKTHSLFFKEKPDYAFVLAENGKQVEIKAEYRRIANQIIVEEMIIA							
AWQPEMPETAQQIHLHQFTKARIQMRKTHSLFFKEKPDYAFVLAENGKQVEIKAEYRRIANQIIVEEMIIA							
330	340	350	360	370	380	390	400
80	90	100	110	120	130	140	
NICAAQFLHEQAKTIGIFNAHSGFDKKYLENAHFI MANLANEQNTELAERYSVENLATIANGYQMRHDIEP							
NICAAQFLHEQAKTIGIFNAHSGFDKKYLENAHFI MANLANEQNTELAERYSVENLATIANGYQMRHDIEP							
410	420	430	440	450	460	470	
150	160	170	180	190	200	210	
IESDYLELRRLRYLTFAEFKSELAPHFGLEGYATWTSPIRKYSDMANHRLIKAVLAKQPYEKPQNDVLAR							
IESDYLELRRLRYLTFAEFKSELAPHFGLEGYATWTSPIRKYSDMANHRLIKAVLAKQPYEKPQNDVLAR							
480	490	500	510	520	530	540	
220	230	240	250	260	270	280	
LQESRRQRLVERDIADWLYCRYLADKVAENVEFNAEQDMRAGLRVQLLENGASLFI PAATLIHNKEEIQ							
LQESRRQRLVERDIADWLYCRYLADKVAENVEFNAEQDMRAGLRVQLLENGASLFI PAATLIHNKEEIQ							
550	560	570	580	590	600	610	

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FIG. 27B

FIG.27B

290 300 310 320 330  
LNPDELALYIKGERIYKIGDIVKVKLITEVKEATRSIVGEILQ  
|||||  
LNPDELALYIKGERIYKIGDIVKVKLITEVKEATRSIVGEILQ  
620 630 640 650 X

; ##cross-references GB:L42023; TIGR:HI1733  
; ##note named as homolog to a protein from Escherichia coli  
; SUMMARY #length 659 #molecular-weight 75782 #checksum 8365

A64139

MFQINPELLAQLKQIHDSEQVEGWKSTDKAYGFLECDKITYFIAPPSMKAMHGDKIKATIEKQGEKE  
QAEPEALIEFMLTRFLAKVRFNKDKKLQVLMHPSINQPIGAQQAQSVKEELOEGDWVAVNLKTHPLRDD  
RFFYATINQLICRADDELAFWVTLARHEQSRYPVRGAEPYEMLDKIRENLITLHFTVIDSESTIMDD  
ALYIEPIAQNSTQIGKLVVAIADPTAVIALDSQIEQAKQRCFTNNVLPFGNIPMLPRELSDCLCSLIAN  
ETRPALVCYIETDLTGNTTAKPHFVSAXVQSKAKLAYNKVSDYLEQALNAWQPEMPETAQQIIMLHQFTK  
ARIQWRKTHSLFFKEKPDYAFVLAENGKQVEIKAEYRRLANQIVFEFAMLIANICAAQFLHEQAKTIGFNT  
HSGFDKFFLENAHNFMANLANEQNQLTELAEYSVENLAITNGYQQRHDIEPIESDYELRLRRYLITFA  
EFKSELAPHFGLGLEGYATWISPIRKYSIMNHLIKAVLAKQPYEKPQND/LARLQEARQNRVVERDI  
ADWLYCRYLADKVASNAEFEEVQDMFRAGLRVQLLENGASLFTPAATLHNNKEIQINPDELALYIKGE  
RTYKIGDMVKVKLITEVKEATRSIVGEILQ

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FIG.28A

Alignment of *H. influenzae* Hia/Hsf and *M. catarrhalis* 200 kDa proteins

	10	20	30	40	50	
MKLEFNTVNTMTQVWSELTRAHTKRASIVAAVLAIVLSATVQA-S						33
.....V.....T.....C.....V.....L.....N.....						32
.....V.....V.....C.....V.....A.....AE.NN						29
.....V.....V.....C.....V.....A.....AE.NN						K22
.....V.....V.....T.....L.....T.....TT						M4071
.....V.....V.....T.....C.....V.....L.....E.NN						11
.....N.....V.....T.....T.....Q.....AE.NS						K9
.....V.....V.....T.....ET.....L.F.....NATDEELDPV						HSF
.....K.....V.....V.....T.....T.....IN						
.....H.YK..F.KA.G.FMA.A.YAKS.STGGSCATCQ.GSVCTLSFARIAALAVLVIGATLS						
.....H.YK..F.KA.G.FMA.A.CAKS.SGGSSSTAGQ.GSSPVRLTRVATLAILVIGATLN						
*** **						
RTAPVLSFHSKGEKTEVNSWGIYFDNKGVLKA						

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TTTTT\*2998660

FIG.28B

API  
Rd  
4223  
LES-1

...RTAPVLSFHSDEGCEKEVTENMGIYFHNKGVILKA-----  
...GTFVKVQSTEDDIEDSAATKDNWQALKAGDTILKA-----  
...GSAYAQQKDTKHIAIGEONQPRRSCTAKADGDRALAIAGENANAQGG  
...GSAYAQN-NSK-AIFGTTCNNN---ASASNEASTAIGSLAKAHAN  
... \* \* \* \* \*

-----  
-----  
-----  
-----  
-----  
-----  
-----

GAITLKAGNLIKIKQNTDESTINASSFTYSLKKDLTDLTSVATEKLSFGANGKVDITSDANG...  
GAITLKAGNLIKIKQ---SINASSFTYSLKKDLTDLTSVATEKLSFGANGKVDITSDANG...  
GKN-LKAKLDQCGKSVTFALAKDLVKTAKVSDTLTIGENTPAGCATP---KVSITSTADG...  
QAIAIGSSNKTVNG-SSLDKIGTDTGQESIAIGGVKASGDASTAIGSDDLHLIDQHENPK...  
QAIAIGGSKPDPNQAANQKAGSHAKGESTAIGGDVLAEGDASTAIGSDDLYLDRNSTNSK...  
\*\* \* \* \* \* \*

33  
32  
29  
K22  
M4071  
11

-----  
-----  
-----  
-----  
-----  
-----  
-----

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[illegible]

FIG. 28C

K9  
HSF  
API  
Rd  
4223  
LES-1

```

...
...LKLAKTGN--VHLGLDSTLPDAVTNIGVLSSS--FTPNDEKTR
...LKLAKTGN--VHLGLDSTLPDAVTNIGVLSSS--FTPNDEKTR
...LKLAKGNDPAVHLGLASTLPDVTNIGASTVT--FSPSDIEKTR
...HPKGTLLNDLNGHAVLKEIRSSKNDVKYRRTTASCHASTA/GAMS
...YPNGLLSTLIQN-HIVLRQIRDSNGSQ-KYRRTAAEGHASTA/GAMA
*          *          *          *          *          *

```

.....

AATVKDVLNAGANNIKGAKTAGCNVESVDLVSAYNNVEFTGDKNILDVLTAKENGKITEVK  
AATVKDVLNAGANNIKGAKTAGCNVESVDLVSAYNNVEFTGDKNILDVLTAKENGKITEVK  
AATIKDVLNAGANNIKGAKVAGCNVESVDLVAGYDNVEFTGDKNILDVLTAKENGKITEVK  
YAQGHFSNAFGTRA-TAKSAYSILAVGLAATAEQOSTIAIGSDATSSSLGAILGAGTRAQIQ...  
YAKGHFANAFGRS-TAEQNYSKAVGLTAKAEKGYTIIATGSAQAQINYGALGALGADTRVDLD...  
\* \* \* \* \*

33 32 29 K22

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	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

**FIG. 28D**

```

M4071
11
K9
HSF
API
Rd
4223
LES-1

```

TENTDEENGLVTAKAVI--DAVNKAGWIVKTTITANGQNGDEFATVASCINVTESGDTTASVT...  
 TENTDEENGLVTAKAVI--DAVNKAGWIVKTTITANGQNGDEFATVASCINVTESGDTTASVT...  
 TENTDEENGLVTAKAVI--DAVNKAGWIVKTTITANGQNGDEFATVASCINVTESGDTTASVT...  
 TETIDEAQA\*

\*RYRNGGLVTKATVI-EAVKSGWRVKTTTANGQNDDEATVAGINVTFANGGTASVT...  
SNSIKRKLIINVAGAVNKTDAVVAQLEAVVKWAKERRITFQGDINSTDVKIGLDNLTIKGG...  
SSTIKRKLIINVAGAYEDTAVVAQLKAIVENLAK-RQITFKGDINGVGKKGIGELTIKGG...  
\* \*\*\*\* \* \* \* \* \* \* \* \*

33

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32  
29  
K22  
M4071  
11  
K9  
HSF  
API  
Rd  
Rd  
4223  
LES-1

[illegible]

FIG. 28E

[illegible]



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33  
32  
29  
K22  
M4071  
11  
K9  
HSF  
API  
Rd  
4223  
LES-1

[illegible]

FIG. 28F

TASEKTVGSGNN-TAELOSGGLTFT-PTTNA-STDKTVGIDGLKFTDNSN-TALEDITT-R...

\*  
\*  
  
\*  
\*  
\*  
\*  
  
\*  
\*  
  
\*  
\*  
  
\*  
\*

.....

.....

.....

.....

.....

...AGRN LKV KQDCANFTYSLQDALIGLTSAITGGI'INGENDA

AGENCIJA KODGANET.VS | ODAI.TGI.TSAT | GETTINGENDA

...ITRDKIGFARD-GDVDE----

... I WANT TO SIGN IN

60 70 ...

-AGSTTGTGINSI NVYCK - NNSNFNSANNSTA

.....

IN--SV..G..A..D..I..II.....

---T.G..S..G.KA..ST..P...A.G..AT...

--N--.PV..K.KA..D-A.F..--I'.....

K NKAT VASGIBAYTDA DM. AT

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Region	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (%)	Urban population growth rate (%)
Asia	1950	1,000	100	10	100	10	1.5	1.5	1.5	1.5	1.5	1.5
	1960	1,200	150	12.5	120	15	2.0	2.0	2.0	2.0	2.0	2.0
	1970	1,400	250	17.9	140	25	2.5	2.5	2.5	2.5	2.5	2.5
	1980	1,600	350	21.9	160	35	3.0	3.0	3.0	3.0	3.0	3.0
	1990	1,800	500	27.8	180	50	3.5	3.5	3.5	3.5	3.5	3.5
	2000	2,000	700	35.0	200	70	4.0	4.0	4.0	4.0	4.0	4.0
	2010	2,200	900	40.9	220	90	4.5	4.5	4.5	4.5	4.5	4.5
	2020	2,400	1,100	45.8	240	110	5.0	5.0	5.0	5.0	5.0	5.0
	2030	2,600	1,300	50.0	260	130	5.5	5.5	5.5	5.5	5.5	5.5
	2040	2,800	1,500	53.6	280	150	6.0	6.0	6.0	6.0	6.0	6.0
	2050	3,000	1,700	56.7	300	170	6.5	6.5	6.5	6.5	6.5	6.5
	2060	3,200	1,900	59.4	320	190	7.0	7.0	7.0	7.0	7.0	7.0
	2070	3,400	2,100	61.8	340	210	7.5	7.5	7.5	7.5	7.5	7.5
	2080	3,600	2,300	63.9	360	230	8.0	8.0	8.0	8.0	8.0	8.0
	2090	3,800	2,500	65.8	380	250	8.5	8.5	8.5	8.5	8.5	8.5
	2100	4,000	2,700	67.5	400	270	9.0	9.0	9.0	9.0	9.0	9.0
	2110	4,200	2,900	69.0	420	290	9.5	9.5	9.5	9.5	9.5	9.5
	2120	4,400	3,100	70.5	440	310	10.0	10.0	10.0	10.0	10.0	10.0
	2130	4,600	3,300	71.7	460	330	10.5	10.5	10.5	10.5	10.5	10.5
	2140	4,800	3,500	72.9	480	350	11.0	11.0	11.0	11.0	11.0	11.0
	2150	5,000	3,700	74.0	500	370	11.5	11.5	11.5	11.5	11.5	11.5
	2160	5,200	3,900	75.0	520	390	12.0	12.0	12.0	12.0	12.0	12.0
	2170	5,400	4,100	75.9	540	410	12.5	12.5	12.5	12.5	12.5	12.5
	2180	5,600	4,300	76.8	560	430	13.0	13.0	13.0	13.0	13.0	13.0
	2190	5,800	4,500	77.6	580	450	13.5	13.5	13.5	13.5	13.5	13.5
	2200	6,000	4,700	78.3	600	470	14.0	14.0	14.0	14.0	14.0	14.0
	2210	6,200	4,900	79.0	620	490	14.5	14.5	14.5	14.5	14.5	14.5
	2220	6,400	5,100	79.7	640	510	15.0	15.0	15.0	15.0	15.0	15.0
	2230	6,600	5,300	80.3	660	530	15.5	15.5	15.5	15.5	15.5	15.5
	2240	6,800	5,500	81.0	680	550	16.0	16.0	16.0	16.0	16.0	16.0
	2250	7,000	5,700	81.4	700	570	16.5	16.5	16.5	16.5		

FIG. 28G

KTVINKDGLTITPAGNGGTINTISBTKGJK..NKAI..VASGLRAYDDA..DVL...AT...
KTVINKDGLTITPAGNGGTINTISBTKGJK..NKAI..VASGLRAYDDA..DVL...AT...
-----
VNNTIGGSNKQIQVGADGIKFADVNVNSNAKFGTTRITEEEIGFAD.....
** *** * ** ***** *
...80                90                100               110              120
...DLANKQDSVYDGLLNLEKGTDKSKFLVADETTATVGNLRKL----
...-----AITDENED..EELEPVQRSV.-----
...E.HVQDA.K.....DN.S.....N.A.....
...E.HVQDA.K.....DN.S.....N.A.....
...AR.F.GA.....DAN.N-L.T.DKA.....
...AE.VQEA.K.....NAS-D.L.E.N.A...D....
...G.H.....N.AN.-L.D.N.A...D....
...RHVEDA.K.....NAN.QP-.T.S.A...D....
...RHVEDA.K.....NAN.QP-.TDS.A...D....
...RHVEDA.K.....NAN.QP-...S.A...D....
...----KQAP.LDKKQ.KVGSVAITTINGI.AGNKKIS.A.GSSANDA
...GKVDFK.P.LDKKQ.QVG.VKIT.DSGINAGDQKISWVKDATDDTIDA
LES-1

	130	140	150	160	
GMVVSTKNSTKEE-SNQVKQADEVLFEQ-KDGVTVTSKSENGKHTVT					...
R.SFKSAKQGTG.QEGTTEV					-----
...L.S..G.RN.K.Y.....T.-SGAA.S.S.KD...I.					.....
...L.S..G.RN.K.Y.....T.-SGAA.S.S.KD...I.					.....

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091936362

項目	単位	1990年	1991年	1992年	1993年	1994年	1995年	1996年	1997年	1998年	1999年	2000年	2001年	2002年	2003年	2004年	2005年	2006年	2007年	2008年	2009年	2010年	2011年	2012年	2013年	2014年	2015年	2016年	2017年	2018年	2019年	2020年	2021年	2022年	2023年	2024年	2025年	2026年	2027年	2028年	2029年	2030年	2031年	2032年	2033年	2034年	2035年	2036年	2037年	2038年	2039年	2040年	2041年	2042年	2043年	2044年	2045年	2046年	2047年	2048年	2049年	2050年	2051年	2052年	2053年	2054年	2055年	2056年	2057年	2058年	2059年	2060年	2061年	2062年	2063年	2064年	2065年	2066年	2067年	2068年	2069年	2070年	2071年	2072年	2073年	2074年	2075年	2076年	2077年	2078年	2079年	2080年	2081年	2082年	2083年	2084年	2085年	2086年	2087年	2088年	2089年	2090年	2091年	2092年	2093年	2094年	2095年	2096年	2097年	2098年	2099年	2100年																																																																		
人口	人	12,000	12,500	13,000	13,500	14,000	14,500	15,000	15,500	16,000	16,500	17,000	17,500	18,000	18,500	19,000	19,500	20,000	20,500	21,000	21,500	22,000	22,500	23,000	23,500	24,000	24,500	25,000	25,500	26,000	26,500	27,000	27,500	28,000	28,500	29,000	29,500	30,000	30,500	31,000	31,500	32,000	32,500	33,000	33,500	34,000	34,500	35,000	35,500	36,000	36,500	37,000	37,500	38,000	38,500	39,000	39,500	40,000	40,500	41,000	41,500	42,000	42,500	43,000	43,500	44,000	44,500	45,000	45,500	46,000	46,500	47,000	47,500	48,000	48,500	49,000	49,500	50,000	50,500	51,000	51,500	52,000	52,500	53,000	53,500	54,000	54,500	55,000	55,500	56,000	56,500	57,000	57,500	58,000	58,500	59,000	59,500	60,000	60,500	61,000	61,500	62,000	62,500	63,000	63,500	64,000	64,500	65,000	65,500	66,000	66,500	67,000	67,500	68,000	68,500	69,000	69,500	70,000	70,500	71,000	71,500	72,000	72,500	73,000	73,500	74,000	74,500	75,000	75,500	76,000	76,500	77,000	77,500	78,000	78,500	79,000	79,500	80,000	80,500	81,000	81,500	82,000	82,500	83,000	83,500	84,000	84,500	85,000	85,500	86,000	86,500	87,000	87,500	88,000	88,500	89,000	89,500	90,000	90,500	91,000	91,500	92,000	92,500	93,000	93,500	94,000	94,500	95,000	95,500	96,000	96,500	97,000	97,500	98,000	98,500	99,000	99,500	100,000

FIG. 28H

..L.S.G.RN.K.Q..H.....	-	-	-	-	-
..L.S.G.RN.K.Q..H.....	-	G.Q.	T.	I.	-
..GKEN.K.Q.....	K.S.G.Q.	T.	AI.	-	-
..G.....	T.-AGAA.....	I.VSVAETKADCGLEKD.....	-	-	-
..G.....	T.-AGAA.....	I.VSVAETKADSGLEKD.....	-	-	-
..G.....	T.-AGAA.....	I.VSVAETKADSGLEKD.....	-	-	-
VTIEQLAAKPTLNAGAGISVTPTEISVDAKSN.	APT.V.	IGVKT.	ELNSDGTSDKF/SVKG.	-	-
VTYKOL.	-	-	-	-	-

33  
32  
29  
K22  
M4071  
11  
K9  
HSF  
API  
Rd  
4223  
LES-1

...GDTIKLKVDNQVNDNLTVGNNGTAVTKGGFETVTKGATDADRGKVT  
 ...GDTIKLKVDNQVNDNLTVGNNGTAVTKGGFETVTKGATDADRGKVT  
 ...GDTIKLKVDNQVNDNLTVGNNGTAVTKGGFETVTKGATDADRGKVT  
 ...SGTNNSLVTAETHASLYLNEWNRTPADSALQSF-TVKEED-DDDANAII  
 .....QVQQADGALQSF-SIRDEK-GQETIISN  
 \* \* \* \* \*

[illegible][illegible]

```

33  -----
32  -----
29  -----
K22 -----
M4071 -----
11  -----
K9   -----
HSF  AGKNLKVRRDGKNITFDLAKNLEVKYAKVSDTLTIGENTPTGTTAT--
API  AGKNLKVRRDGKNITFDLAKNLEVKYAKVSDTLTIGENTPTGTTAT--
Rd   AGKNLKVRRDGKNITFDLAKNLEVKYATFTSDRLTIG-----
4223 -----EQIQVGANGT.FTNWNGSNPGTIGIANTARITRDKIGFAGSDGAVDINK
LES-1 IEQVASGN-.T...IR-----

```

FIG. 28J

[illegible]

[illegible][illegible][illegible]

33  
32  
29  
K22  
M4071  
11  
K9  
HSF  
API  
Rd

[illegible]

...IAENLNLAKEIHTTKGTADTALQTFIVKKVDENNADDANA.IT-----4223  
 ...IAENLNLAKEIHTTKGTADTALQTFIVKK----DGATDDEIT-----LES-1  
 ...\*\*\* \*\* \* \* \*

VKYDVNVGDGLKIGDDKKIVADITTLIVTGEKVSVIPAGANSWNNKKLVNREGLATALANLS...  
VKYDVNVGDGLKIGDDKKIVADITTLIVTGEKVSVIPAGANSWNNKKLVNREGLATALANLS...  
VGQKVANNQ--VNILTLKGENGILNIKTDKNGIVTFGIN--  
VGRDGTQNGKTVNHLKLKGENGLJTVAINKDGI VTFGIN--  
\* \* \* \* \*

33  
32  
29  
K22  
M40  
11

FIG. 28M

WTAKADYAGESEGETDQEVKAGDKVTF-KAGKNLKVQSEKDFYSLQD  
-----  
.....  
-----TTSGLKAGKST-LNDGLSHIKPTCSSEQIQVGADG  
-----TQSGLKAGDSHTLNKGDKSIKNPASNEDIQVGADG  
\*\*\*\*\* \* \*\* \* \* \*

.....

TLTGLTSLITLGGTANGRNDGTIVNKDGLTITLANGAAAGTDAENGT-----ISVTKDGLISA...  
TLTGLTSLITLGGTANGRNDGTIVNKDGLTITLANGAAAGTDAENGT-----ISVTKDGLISA...

```

VKFAKVNNGVVGAGIDGTRITRDEIGFTGNGSLDKSPHL-----SLDGINA
VKFAKVDK-GNSSTGIDGTSRTIKQIGFTGANGSLDTTKPHLTKDKLKVEGEVEITNIGINA
+      **      *      *      *      *      *      *      *      *

```

.....



K9  
HSF  
API  
Rd  
4223  
LES-1

33 32 29 K22

FIG. 28N

```

...
GKKEITNVKSA--LKTYKDTONTA
GKKEITNVKSA--LKTYKDTONTA
...
GKKKTINIQSELAQNSHDAVTGGKYDYLKT
GKKKTINIQSGDITQNSNDAVTGGRYDYLKT
* * * * *

```

GATQPAANTAIEVAKQDLVDLITKYPATGAAGNCADAKAPDTTAA TVGDLRGLGWLSAKKTAE...  
-DE...  
EL...  
EL...  
\*  
.....  
.....  
.....  
.....

***SUBSTITUTE SHEET (RULE 26)***

186/204

M4071  
11  
K9  
HSF  
SPI  
Rd  
4223  
LES-1

33 32 29

[illegible]

FIG. 280

```

...
...
...
...TODKEFHAAV/KVANEVEFEVGKNGATV/SAKT
...TODKEFHAAV/KVANEVEFEVGKNGATV/SAKT
...
...ENKISSTAKTAQNSLHEFSVADEQGNFTV
...ESKINSAAKTAQNSLHEFSVADEQGNFTV
...
...
--ISVTKGSPAENVKT..
--ISVTKGSPAENVKT..
...
...
DNINGKHVTID/AEAKVGDGLEKDTGDKIKLI/VNVDGNLLI/VDATKGAS/VAKGFNAVIT.
DNINGKHVTID/AEAKVGDGLEKDTGDKIKLI/VNVDGNLLI/VDATKGAS/VAKGFNAVIT.
SNPYSSYDTSKTS/DVITFAGENGITTKVNKGWVR/GIDQTKGLTPKLIVGNNCKGIVIDS..
SNPYSSYDTSKTS/DVITFAGENGITTKVNKGWVR/GIDQTKGLTPKLIVGNNCKGIVIDS..
*      *      *      *      *      *      *      *      *      *

```

[illegible]

K22  
M4071  
11  
K9  
HSF  
API  
Rd  
LES-1

.. DATTCGVNAD-RGVK-~~---~~AEDENGADV/DKKV-  
 ..  
 ..  
 ..  
 ..  
 .. DATTAQGTNANERGVVWKGSGCATATET/DKKV-  
 .. DATTAQGTNANERGVVWKGSGCATATET/DKKV-  
 .. QNGQVITIGLSNITLANVINDKGSV/RTTEQENIKDEKTRA  
 .. KDGQVITIGLSNITLANVINDGAGHSLS-ÖGLAN-DIDKTRA  
 \*

[illegible]

FIG.28Q

FOOTPRINT 29895660

33  
32  
29  
K22  
M4071  
11  
K9  
HSF  
API  
Rd  
4223  
LES-1

-----FALANDLVKNATVSDKLSLGANGKKVIDITSANG-----  
...D--FTYS.KKE.KNLTVEITE...F...N...-----  
...GKSVT...K.D.TS.K...I.KDIN...-----  
...GKSVT...K.D.TS.K...I.KDIN...-----  
...T.EK...N...T...-----  
...K.G.T...T.TI.GGAAAGAT.TPKNVTSTTDG  
...K.SMRT...T.TI.GSTTIGSA.TPKNVTSTASG  
...-KNIT...S.S...T.N.N...TK...  
...-KNIT...S.S...T.N.N...TK...  
...N...T...  
...IEVK-DKILGVKTTTITSTIGCANKFALSQAATGALVKASDIVA--  
...IEVTSKILGVKTTTITSTIGCANKFALSQAATGALVKASDIAT--  
... \* \* \* \*

210 220 230 240 250  
LKFAKQGT-NGQNEV--VHLNGIASLTDPRVGKTAHLITKEISDIERN--RAASVGDVINA...  
...L.T.NG...S...T.TLA.T.G.VDTN.DAVNH...Q...S...  
...L.T.NG...T.TIT.MT.QASNGVAVQ-NH...A...  
...L.T.NG...T.TIT.MT.QASNGVAVQ-NH...A...  
...PS...T.TIT.TIKSATNGVDVQNH...A...  
...DAA--A.DIT...G...T.TK.SPAT.IDGDDQS.HYT--IK...  
...V...GA.GANGDTT--TN...Q.TLNGVWSKLDGNGITADEKK...Q...S...  
...DSKT--DDA--I...T.TLNGGATTNLCGNGITNEKK...K...  
...X.DSKT--DDA--I...T.TLNGGATTNLCGNGITNEKK...K...  
...P...T.TLNGGATTNLCGNGITNEKK...K...  
...P...T.TLNGGATTNLCGNGITNEKK...K...

Run	Time (h)	Temp (°C)	Pressure (atm)	Flow (ml/min)	Conc (g/l)	Yield (%)	Viscosity (dl/g)	Color	Notes
1	1.0	100	1.0	1.0	0.1	0.1	0.1	Colorless	Initial run
2	2.0	100	1.0	1.0	0.2	0.2	0.2	Colorless	
3	3.0	100	1.0	1.0	0.3	0.3	0.3	Colorless	
4	4.0	100	1.0	1.0	0.4	0.4	0.4	Colorless	
5	5.0	100	1.0	1.0	0.5	0.5	0.5	Colorless	
6	6.0	100	1.0	1.0	0.6	0.6	0.6	Colorless	
7	7.0	100	1.0	1.0	0.7	0.7	0.7	Colorless	
8	8.0	100	1.0	1.0	0.8	0.8	0.8	Colorless	
9	9.0	100	1.0	1.0	0.9	0.9	0.9	Colorless	
10	10.0	100	1.0	1.0	1.0	1.0	1.0	Colorless	
11	11.0	100	1.0	1.0	1.1	1.1	1.1	Colorless	
12	12.0	100	1.0	1.0	1.2	1.2	1.2	Colorless	
13	13.0	100	1.0	1.0	1.3	1.3	1.3	Colorless	
14	14.0	100	1.0	1.0	1.4	1.4	1.4	Colorless	
15	15.0	100	1.0	1.0	1.5	1.5	1.5	Colorless	
16	16.0	100	1.0	1.0	1.6	1.6	1.6	Colorless	
17	17.0	100	1.0	1.0	1.7	1.7	1.7	Colorless	
18	18.0	100	1.0	1.0	1.8	1.8	1.8	Colorless	
19	19.0	100	1.0	1.0	1.9	1.9	1.9	Colorless	
20	20.0	100	1.0	1.0	2.0	2.0	2.0	Colorless	
21	21.0	100	1.0	1.0	2.1	2.1	2.1	Colorless	
22	22.0	100	1.0	1.0	2.2	2.2	2.2	Colorless	
23	23.0	100	1.0	1.0	2.3	2.3	2.3	Colorless	
24	24.0	100	1.0	1.0	2.4	2.4	2.4	Colorless	
25	25.0	100	1.0	1.0	2.5	2.5	2.5	Colorless	
26	26.0	100	1.0	1.0	2.6	2.6	2.6	Colorless	
27	27.0	100	1.0	1.0	2.7	2.7	2.7	Colorless	
28	28.0	100	1.0	1.0	2.8	2.8	2.8	Colorless	
29	29.0	100	1.0	1.0	2.9	2.9	2.9	Colorless	
30	30.0	100	1.0	1.0	3.0	3.0	3.0	Colorless	
31	31.0	100	1.0	1.0	3.1	3.1	3.1	Colorless	
32	32.0	100	1.0	1.0	3.2	3.2	3.2	Colorless	
33	33.0	100	1.0	1.0	3.3	3.3	3.3	Colorless	
34	34.0	100	1.0	1.0	3.4	3.4	3.4	Colorless	
35	35.0	100	1.0	1.0	3.5	3.5	3.5	Colorless	
36	36.0	100	1.0	1.0	3.6	3.6	3.6	Colorless	
37	37.0	100	1.0	1.0	3.7	3.7	3.7	Colorless	
38	38.0	100	1.0	1.0	3.8	3.8	3.8	Colorless	
39	39.0	100	1.0	1.0	3.9	3.9	3.9	Colorless	
40	40.0	100	1.0	1.0	4.0	4.0	4.0	Colorless	
41	41.0	100	1.0	1.0	4.1	4.1	4.1	Colorless	
42	42.0	100	1.0	1.0	4.2	4.2	4.2	Colorless	
43	43.0	100	1.0	1.0	4.3	4.3	4.3	Colorless	
44	44.0	100	1.0						

FIG. 28R

[illegible]

310	320	330	340	350	360
KKTTVRVDVTGLPVOYVTEDSKTVKVGNEYTEAKQGSADMDKV-ENGKLAKT/KLVSA...					
.....G.....	K.D.....	NQ.....	E.....		
.....G.....	D.K.....	E.....			
.....G.....	D.K.....	E.....			
.....GE.....					
.....F.....	G.....	-K.E.V.....			

FIG. 28S

FIG. 28S

.ENK. TE. KIGAKTS. IKEKOKLFT. KANK. TNKVDG. NATEDA-DE.. GLV. AKDVID....  
ESNGKSTK. KIGAKTSIGIKEKOKLFT. KANKOIN. VASNNAADDI-DE.. GLV. AETVIN....  
.DNK. TE. KIGAKTS. IK. HNGKLT. K. LKD. NNN. VIVTETDGKOE. NGLV. AKAVID....  
.DNK. TE. KIGAKTS. IK. HNGKLT. K. LKD. NNN. VIVTETDGKOE. NGLV. AKAVID....  
.....  
..QGINEINAFVKGLEKASDNKTKNAAVTVGDINAVAGTPLTFAG-DT. TT. KLGETLTI...  
..QGINEINAFIKGLENAKDKTKNAAVTVGDINAVAGTPLTFAG-DT. TT. KLGETLTI...  
\*\* \*

... 370 380 390 400  
...NGINPVKISNADGTEDTDAVSFKQKALQDKQVTLAS  
...S.....T.  
...S.Q.....E..EN.....E.....T..  
...S.Q.....E..EN.....E.....T..  
.....N.....  
.....E.....N.....  
...VNKTGR. KTTDANGQNG. ---FATVAGINVTF---  
...VNKAGR. KTTGANNQAGQ---FEITVSGINVTF---.D  
...VNKAGR. KTTGANGQND. ---FATVAGINVTF---.D  
...VNKAGR. KTTGANGQND. ---FATVAGINVTF---.D  
.....  
...KGGQIDTNKLTNNIGVAGTDGFTV. LAK. LTNLN. VN  
...KGGQIDTNKLTNNIGVAGTDGFTV. LAK. LTNLN. VN  
...

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K22  
M4071  
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K9  
HSF  
API  
Rd  
4223  
LESS-1

FIG. 28T

FIG. 28T

NAYANGSDADGGKATQITLGNLNFKEFKSTDSSELNKAAGDITVTPKKGSVQVGGDKAT...  
...T.N.....S.G.....S.G..K.S.T.....S..  
...N.....N.G.....G.....VEN.....E..  
...N.....N.G.....G.....VEN.....E..  
...GI...S.G.....G.....EN..  
...V.V.....S.G.....G.....DK...I..  
GNGTTATVING-TDGIITVKYDAKVGDLKLDG-KIADTTALTIVNDGNANPKGVADVA..  
GNGTTAVTGDATNGITVKYKVGDLKIGNDQKITADTTALTIVTGGK-----VTAPD..  
GNGTTAEVTKANDGSITVKYKVGDLKLDG-KIVADTTVLTVADGK-----VTAPN..  
GNGTTAEVTKANDGSITVKYKVGDLKLDG-KIVADTTVLTVADGK-----VTAPN..  
...G.....S.G.....G.....EN..  
AGGTTKIDDKGVSF-----  
AGGTTIRIDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDINDAVNFKQFNEVAK...  
\* \* \*

... 470 480 490 500  
...IQDGAKTITGLVEASELVDLSINKLGMKVGKDGTCG---AT  
...SK.N.E.....E.....E.V.S.---EL  
...N.T...D.....E.....D.S.---EL  
...N.T...D.....E.....D.S.---E..  
...T.T.....V..  
...STDEK-----T.KG..TA..S.S.TTTAAEADG.---TL  
...ATNGKK-----N.G.A.A...S.TAK-AEADTANGGEL  
...NGDGKK-----F.D.G.A.A...S.TATA..E.---EV  
...NGDGKK-----F.D.G.A.A...S.TATA..E.---EV

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29  
K22  
M4071  
12  
11  
K9  
HSF  
API





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FIG.28V

M4071  
12  
11  
K9  
HSF  
API  
Rd  
4223  
LES-1

TTTTT 29E9E6E0

.....G- GA.G.NT.NT.S---.TK.  
.....R.SG-  
.....N. ....G- --G.NN.NT.S---.TK. ....DQS.  
.....N. ....G- --G.NN.NT.S---.TK. ....DQS.  
.....G- GA.G.NT.NT.S---.TK.  
.....G- GA.G.NT.NT.S---.TK.  
.....F. ....G- .....R.  
.....VD...KP. D.DKL. L. HGKPLDACHQV...L.-GNSD-.I  
\* \*\*\* \* \* \* \* \*\* \* \* \* \*

610 620 630 640 650 660 ...  
KNVWSGLKFGDANFNPLTSSADNLTKQYDNAYKGLJNLDEKSKGKQPTPVADNTAATVGD...  
.....D. ....GAD...L.  
.....D. ....GAD...L.  
.....D.  
.....D. ....N.D. ....GTD...V.  
.....D. ....GAD...L.  
T. ....CHTLANGTV..FE-H. ....D. ....GADNN-  
T. ....CHTLANGTV..FE-H. ....XD. ....GADNN-  
.....  
.....  
.....TLTNIKSTLP.I.TPNT.NA.AGQAQSLPISLSAAQSN..S.K.V...

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FIG.28W

TABLE 28W

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29  
K22  
M4071  
12  
11  
K9  
HSF  
API  
Rd  
4223  
LES-1

670 680 690 700  
... TGLGWISADKTTGES-KEYSAQRNANEVKFKSGNGIN  
...  
... IN...N...H  
... IN...N...H  
... K...IN...N...  
...  
... G...T...HD...  
... LD...N...  
... FNQ...N...  
... FNQ...N...  
...  
...  
... INV.FNLQTNHNOQDEV.A.DIVNFVANGTGADITSVRS  
... \*\*\* \* \*\* \*

710 720 730 740 750 760 ...  
VSKTLDNGTREITFELAKDENAIAPGSGKALRDNIVAIGIGNWNNAKSGAFGDPWIED...  
...  
... V...R...Y...  
... V...R...Y...  
...  
... V...R...G...

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K22  
M4071  
12  
11  
K9  
HSF  
API  
Rd  
4223  
LES-1

[illegible]

**FIG. 28X**

$$\begin{array}{l} \dots V \dots R \dots G \dots \\ \dots - \dots V \dots G \dots \\ \dots - \dots V \dots G \dots \end{array}$$

...KAKD. KEYKA. DIMPN. SLKACKSASDAKTPTGLSLVN...

**	*
* * *	*
770	780
... ..	*
790	*
800	*

KAGGSYA FGNDRITSKNTFVLGNGVNAKYKANGKVDT-----

S...RD...N.L.EE-

.....

.....

.....

.....

.....

.....

.....

.....

...PNA.KGST.DAVALNNLSKA.FKSKDGT'TT'TVSSDGISIQ

\*  
 \*  
 \*  
 \*  
 \*  
 \*  
 \*  
 \*  
 \*  
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.....

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***SUBSTITUTE SHEET (RULE 26)***

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FIG. 28Y

$\alpha$	$\beta$	$\gamma$	$\delta$	$\epsilon$	$\zeta$	$\eta$	$\theta$	$\iota$	$\kappa$	$\lambda$	$\mu$	$\nu$	$\xi$	$\omicron$	$\pi$	$\rho$	$\sigma$	$\tau$	$\upsilon$	$\phi$	$\chi$	$\psi$	$\omega$	$\Omega$	$\Theta$	$\Phi$	$\Psi$	$\Sigma$	$\Pi$	$\Lambda$	$\Gamma$	$\Delta$	$\nabla$	$\Xi$	$\Upsilon$	$\Zeta$	$\Eta$	$\Theta$	$\Iota$	$\Kappa$	$\Lambda$	$\Mu$	$Nu$	$\Xi$	$Omicron$	$Pi$	$Rho$	$Sigma$	$Tau$	$Upsilon$	$Phi$	$Chi$	$Psi$	$Omega$																																													
0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

VVKSNEFTVKETNGKETSLVKVGDLYYSKEDI DLITGQPKLDGNIVAAKYQDKCKKWS-V.  
VVKSNEFTVKETNGKETSLVKVGDLYYSKEDI DPATGKPKVINENAVAAKYQDKCKKWSAD..  
VVKSNEFTVKNA DSGSETNLVKVGDLYYSKEDI DPATSKPMTGKITE---- KYKVENGKAVSAN  
VVKSNEFTVKNA DSGSETNLVKVGDLYYSKEDI DPATSKPMTGKITE---- KYKVENGKAVSAN..  
VDSSGOAKANTPVL SANGLD LGCKVI SNVKGTKTDIDAANVOQL NEVRNLL GLGNAGCNDAD...  
DNSSI-----TL SKDGLNVCGKVI SNVKGTKTDIDAANVOQL NEVRNLL GLGNAGCNDAD... \* + \* + \*

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API  
Rd  
4223  
LES-1

..TTNTEATITNKGSGYVTGNQ-----  
 ..GSSNTAVTLTNKGYVTGNQ-----  
 ..GSK-TEVTLTNKSGSYVTGNQ-----  
 ..GSK-TEVTLTNKSGSYVTGNQ-----  
 ..-----  
 ..GNGVNIADIKDPNCGSSSNRTVIKAGTIVLGCKGNNDT  
 ..GNGVNIADIKDPNCGSSSNRTVIKAGTIVLGCKGNNDT

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Case	Age	Sex	Duration of illness	Onset	Course	Outcome
1	10	M	10 days	Acute	Recovery	Good
2	12	F	15 days	Acute	Recovery	Good
3	15	M	20 days	Acute	Recovery	Good
4	18	F	25 days	Acute	Recovery	Good
5	20	M	30 days	Acute	Recovery	Good
6	22	F	35 days	Acute	Recovery	Good
7	25	M	40 days	Acute	Recovery	Good
8	28	F	45 days	Acute	Recovery	Good
9	30	M	50 days	Acute	Recovery	Good
10	32	F	55 days	Acute	Recovery	Good
11	35	M	60 days	Acute	Recovery	Good
12	38	F	65 days	Acute	Recovery	Good
13	40	M	70 days	Acute	Recovery	Good
14	42	F	75 days	Acute	Recovery	Good
15	45	M	80 days	Acute	Recovery	Good
16	48	F	85 days	Acute	Recovery	Good
17	50	M	90 days	Acute	Recovery	Good
18	52	F	95 days	Acute	Recovery	Good
19	55	M	100 days	Acute	Recovery	Good
20	58	F	105 days	Acute	Recovery	Good
21	60	M	110 days	Acute	Recovery	Good
22	62	F	115 days	Acute	Recovery	Good
23	65	M	120 days	Acute	Recovery	Good
24	68	F	125 days	Acute	Recovery	Good
25	70	M	130 days	Acute	Recovery	Good
26	72	F	135 days	Acute	Recovery	Good
27	75	M	140 days	Acute	Recovery	Good
28	78	F	145 days	Acute	Recovery	Good
29	80	M	150 days	Acute	Recovery	Good
30	82	F	155 days	Acute	Recovery	Good
31	85	M	160 days	Acute	Recovery	Good
32	88	F	165 days	Acute	Recovery	Good
33	90	M	170 days	Acute	Recovery	Good
34	92	F	175 days	Acute	Recovery	Good
35	95	M	180 days	Acute	Recovery	Good
36	98	F	185 days	Acute	Recovery	Good
37	100	M	190 days	Acute	Recovery	Good
38	102	F	195 days	Acute	Recovery	Good
39	105	M	200 days	Acute	Recovery	Good
40	108	F	205 days	Acute	Recovery	Good
41	110	M	210 days	Acute	Recovery	Good
42	112	F	215 days	Acute	Recovery	Good
43	115	M	220 days	Acute	Recovery	Good
44	118	F	225 days	Acute	Recovery	Good
45	120	M	230 days	Acute	Recovery	Good
46	122	F	235 days	Acute	Recovery	Good
47	125	M	240 days	Acute	Recovery	Good
48	128	F	245 days	Acute	Recovery	Good
49	130	M	250 days	Acute	Recovery	Good
50	132	F	255 days	Acute	Recovery	Good
51	135	M	260 days	Acute	Recovery	Good
52	138	F	265 days	Acute	Recovery	Good
53	140	M	270 days	Acute	Recovery	Good
54	142	F	275 days	Acute	Recovery	Good
55	145	M	280 days	Acute	Recovery	Good
56	148	F	285 days	Acute	Recovery	Good
57	150	M	290 days	Acute	Recovery	Good
58	152	F	295 days	Acute	Recovery	Good
59	155	M	300 days	Acute	Recovery	Good
60	158	F	305 days	Acute	Recovery	Good
61	160	M	310 days	Acute	Recovery	Good
62	162	F	315 days	Acute	Recovery	Good
63	165	M	320 days	Acute	Recovery	Good
64	168	F	325 days	Acute	Recovery	Good
65	170	M	330 days	Acute	Recovery	

FIG. 28Z

✱  
✱  
✱  
  
✱

VADAIKSGFEKGKADEADAKRAFDD--KITKALSAGITE-IVNAHDKVRFANGINTKV/SAAT...  
VADAIKSGFEKGKADEAEKAAAFGD--ETKALSSDKLE-TVNANDKVRFANGINTKV/SAAT...  
VADAIKSGFEKGKADAEEAEKAFESAOKQLSOKAE-TVNAHDKVRFANGINTKV/SAAT...  
VADAIKSGFEKGKADAEEAEKAFESAOKQLSOKAE-TVNAHDKVRFANGINTKV/SAAT...  
EKLATGIGVGV/DKDCANNGDLSNVWKTQKDGSKKALLATYNAAGQTNYLTNNPAEAI DRI...  
EKLATGIGVGV/DKDCANNGDLSNVWKTQKDGSKKALLATYNAAGQTNYLTNNPAEAI DRI...  
\* \* \*

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M4071  
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K9  
HSF

... VESTDANGDKVITTFVKTDVELPLTQIYNTDANGKIKTKW  
... VESTDANGDKVITTFVKTDVELPLTQIYNTDANGKI---V  
... VESTDANGDKVITTFVKTDVELPLTQIYNTDANGKI---V

API  
Rd  
4223  
LES-1

33  
32  
29  
K22  
M4071

[illegible]

FIG. 28A'

VESTDANGDKVTTTFVKTDVELPLTQIYNTDANKKI--V  
.....  
NEQGIRFFHHNDGNQEPFWQGRNGIDSSASGKHSAVTGFQ-  
.....  
NEQGIRFFHHNDGNQEPFWQGRNGIDSSASGKHSAVTGFQ-  
.....

KDCQTKWYELNADGTADMTKEVTLGNVSDGKKVKDNG---KWIHAKADGTADTKTGEVD.  
 KNGD-KWYTKDDGSTDMTKEVTLGNVSDGKKVKEDN----KWYGVKSDGSTDKTQVVEE.  
 KKADGKWYELNADGTASN-KEVTLGNVDANGKKVKV/TENGADKWYTYTNADGAADTKGEVS.  
 KKADGKWYELNADGTASN-KEVTLGNVDANGKKVKV/TENGADKWYTYTNADGAADTKGEVS.  
 AKADGEAAVAIGRQTQACNQSIAGINNAQATGDSIAIGTGNVAGKHSGAIGDPSTVKADN..  
 AKADGEAAVAIGRQTQACNQSIAGINNAQATGDSIAIGTGNVVTGKHSGAIGDPSTVKADN..  
 \*\* \* \* \* \* \* \* \* \* \* \*  
 .....  
 .....  
 .....  
 .....  
 .....

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Rd  
4223  
LES-1

33 32 29

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

**FIG. 28B,**

[illegible]

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K22  
M4071  
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HSF  
API  
Rd  
4223  
LES-1

[illegible]

**FIG. 28C,**

910	920	930	940	950	...
AINGSOLYAVAKGVINLAGOVN-----	KVKKRADAGTASALAAQOLPQASWCKSWISIA...				
.....	NLEKVN.....	T.P.....			
.....	.....	P.....			
.....	.....	P.....			
.....	.....	P.....			
.....	.....	P.....			
.....	NLEKVN.....	T.P.....	A.....		
.....	NLEKVN.....	T.P.....			
.....	NLEKVN.....	T.P.....	A.....		
.....	NLEKVN.....	T.P.....	A.....		
.....	.....	P.....			
V.....	ATQSI NAT.ELDHRIHQENK.N. IS. M.MASM. YIP.R. TGG.....				
V.....	ATQGI NAT.ELDHRIHQENK.N. IS. M.MASM. YIP.R. TGG.....				
*****	** ** *	*****	*****	*****	*****



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SEQ	ID	NO:56
SEQ	ID	NO:55
SEQ	ID	NO:59
SEQ	ID	NO:58
SEQ	ID	NO:57

**FIG. 28D,**

...	960	970	980	990	1000	
...	GSSYQOQSGLAIGVSRISDNEKVIIRLSGTINSQEKTVGAAGVGVM*					33
...	N.....					32
...	N.....					29
...	N.....					K22
...	N.....					M4071
...	L.....					12
...	N.....					11
...	N.....					K9
...	N.....					HSF
...	N.....					API
...	N.....					Rd
...	IATHN. GAV. V. L. KL. . . . . QWVFKIN. SADD. . . . . HV. A. V. A. FHF*					4223
...	IATHN. GAV. V. L. KL. . . . . QWVFKIN. SADD. . . . . HV. A. V. A. FHF*					LFS-1
...	*****	*****	*****	*****	*****	

**FIG. 29**

Oligonucleotides primers to PCR amplify truncated strain 11 S44 hia gene.

Node I

5' M S44A T V E A N N T 3' 6817.SL

# sty I

H T I T F A L A K D L G  
 CACACATTACCTTTCCTTTACGGAATACCTTGGT  
 GGTGGTATTCGAAACGAAATGCTTTCCTTTCGTAACCACTTACGGC

SEQ	ID	NO: 59
SEQ	ID	NO: 58
SEQ	ID	NO: 57

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FIG. 30A

Construction of JB-2930-3, pBR T7/S44 hia(11)/cer/kanR

PCR amplify Nde-Sty S44 hia (11)  
clone into pCR II

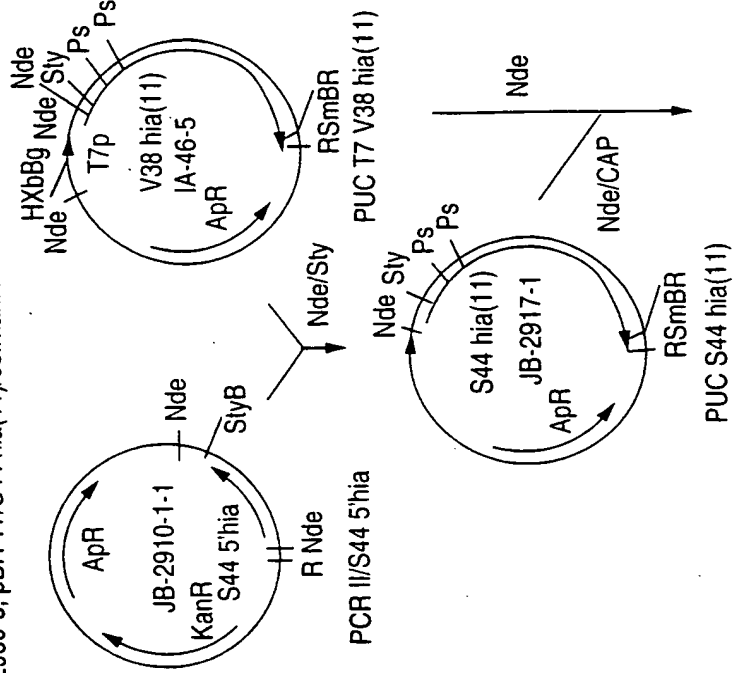


FIG. 30A

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TOP SECRET

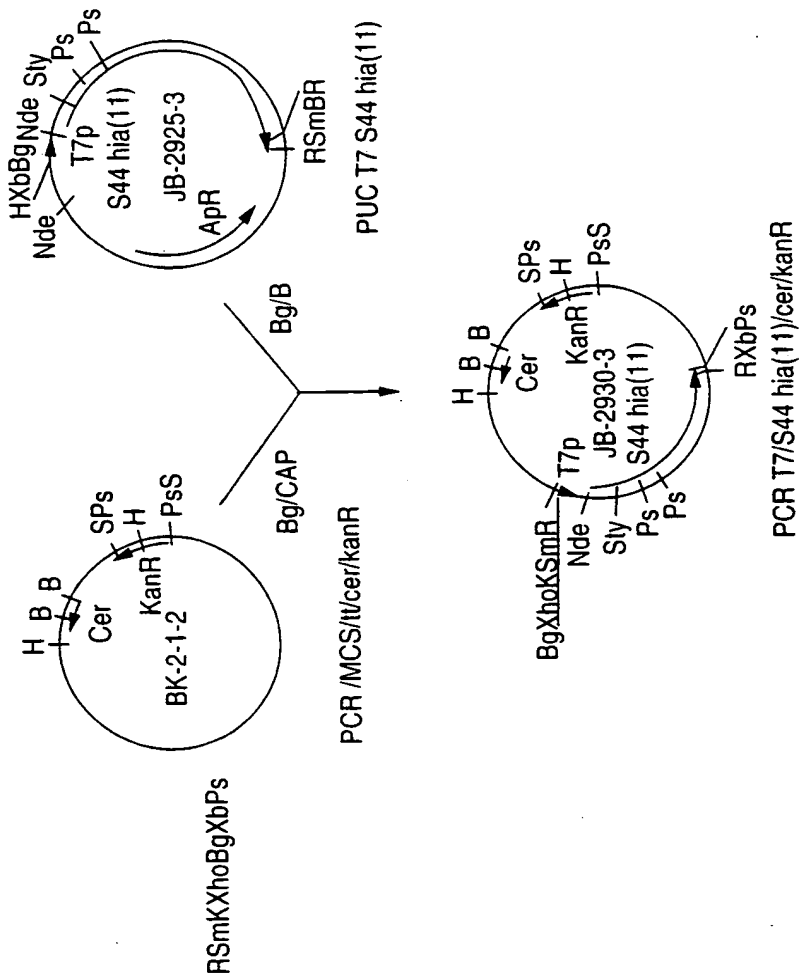


FIG.30B

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Production of S44 rHia from different vectors

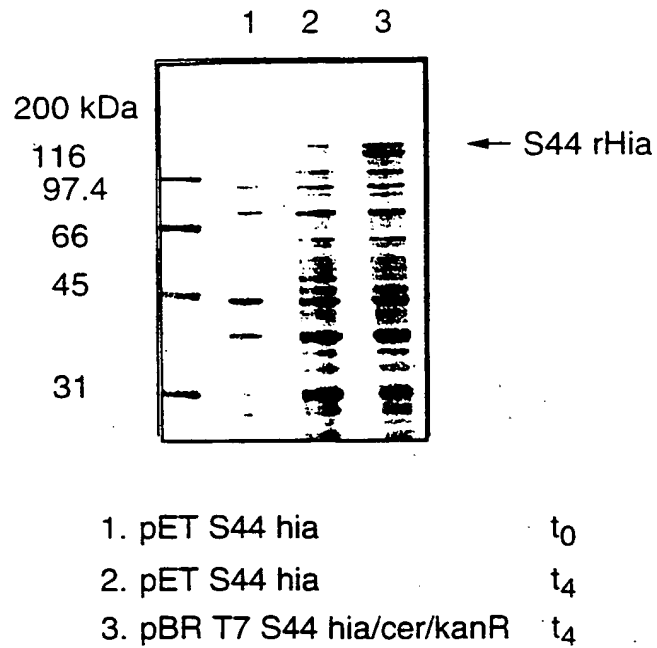


FIG.31

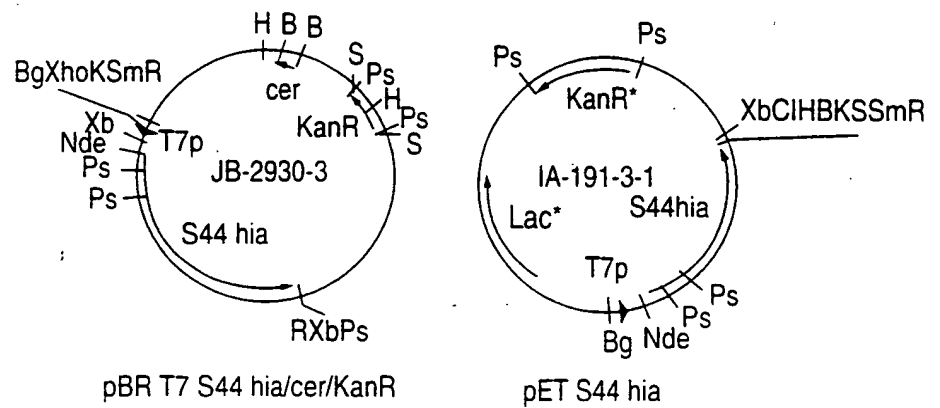


FIG.32